Scoring table:

Searched:

Database

Result Š Perfect score: Sequence:

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Sequence 2, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 3, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 0, 5270178
Patent No. 5270178
Patent No. 5270178
Patent No. 5270178
             Sequence Sequence S
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Sequence 2, Application US/08981088

Patent No. 6146824

GENERAL INFORMATION:
APPLICANT: BAR-SHAVIT, RACHEL
APPLICANT: BAR-SHAVIT, RACHEL
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
ITTLE OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
STREET: VA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 6; Leuy-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CORERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORILE Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,088
FILING DATE: 27-JAN-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: OLIFF, JAMES A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Carney, Darrell H.;Gleno, Kevin C.
TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES;COMPOSITIONS AND METHODS FOR USE
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,201
FILING DATE: 31-OCT-1986
             US-07-720-189-1
US-09-665-872-2
US-09-667-570A-2
US-09-667-570A-1
US-08-295-471-1
US-08-955-471-1
US-09-667-570A-3
US-08-756-506-4
US-08-756-506-4
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s; Pred. No. 0.00
0; Mismatches
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5270178-2
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Best Local Similarity 100.
Matches 10; Conservative
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;Patent No. 5352664
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SEQ ID NO:3
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                                                                                                                                                  May 12, 2003, 15:33:37 ; Search time 9.6 Seconds (without alignments) 30.649 Million cell updates/sec
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Sequence 52,
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Sequence 5
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Sequence 8
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/cgn2_6/ptcdata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/PCTUS_COMB.pep:*
                          GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-338-364-8

US-08-38-368-2

US-08-558-269-10

US-09-410-882-10

US-09-410-812-10

US-09-955-471-4

US-08-955-471-4

US-09-972-11

US-09-972-3

US-09-11357-3

US-09-518-046-25

US-09-518-046-25

US-09-518-046-25

US-09-518-046-25

US-09-952-967-8

US-09-518-046-25

US-09-952-967-8

US-09-952-967-8

US-09-952-967-8

US-09-968-944-483-51

US-09-900-944-681-51

US-09-944-681-51

US-08-944-483-51
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5270178-20
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM protein - protein search, using sw model
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Gapop'10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Gaps

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FILING DATE:
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            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                       COMPUTER:
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USEFUL FOR DETECTING AND TREATING DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: CARRY, DARRELL H.
APPLICANT: RAMARKISHNAN, SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHEP:002
CURRENT APPLICATION NUMBER: US,08/330,594C
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial, Sequence: Synthetic OTHER INFORMATION: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                       Mismatches
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REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 40455
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANDADOS, EDWARD N.
KLASS, MICHARL R.
RUSSELL, JOHN C.
STEWART, KENT D.
STEWART, KENT D.
STEWARTONE, STEVEN D.
NVEWITON: NOVEL SERINE PROT
NVEWITON: OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08330594C Patent No. 6184342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/08944483 Patent No. 6232456
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                 TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1994-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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NO
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                         linear
                                                                                                                                          TYPE: amino acid
STRANDEDNESS: s1
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                                                                                                                                                                             ; TOPOLOGY: 11:
; MOLECULE TYPE:
; HYPOTHETICAL: 1
US-08-981-088-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-330-594-8
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APPLICANT:
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NOVEL POLYPEPTIDES AND COAGULATION THERAPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 4;
100.0%; Pred. No. 0.038;
tive. 0; Mismatches
                                                                                                                                            OPERATING SYSTEM: DOS
SUFTWARE: FRSESED for Windows Version 2.0
SUFTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/338,368
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: GILEAD SCIENCES, INC. 353 LAKESIDE DRIVE
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APPLICANT: GIBBS, CRAIG S.
APPLICANT: LEUNG, LAWRENCE L.K.
APPLICANT: TSIANG, MANUEL
TITLE OF INVENTION: NOVEL POLYPI
TITLE OF INVENTION: THERAPY
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: No. 6232456e
US-08-944-483-52
                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                       TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 amino acids
                                                                                                                                                                                                                                                                                                                                            NAME: Becker, Cheryl L
REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                       Diskette
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                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                      ZIP: 60064-3500
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
Abbott Par
                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOSTER CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                          USA
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APPLICATION NUMBER: US 08/258,038

318 CEGDSGGPFV 327

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Serine Protease-Derived Polypeptides and
Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mesters, Serine Processing Applicant: Mesters, Serine Processing Serine Processing TITLE OF INVENTION: Anti-Peptide Antibodies, Julius OF INVENTION: for Inhibiting Coagulation NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r: 10666 No. 5679639th Torrey Pines Road, TPC La Jolla
                                                                                                                                 GENERAL INCORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
ONNERS OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 59; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/410,882
                                               US-09-410-882-10
: Sequence 10, Application US/09410882
: Patent No. 6287561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08295411 Patent No. 5679639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: CR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                John H.
Rolf M.
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTK: ...
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 376 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII (text) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-410-882-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Griffin,
APPLICANT: Mesters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 CEGDSGGPFV 327
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: 1
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALXSTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 59; DB 2; L
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 59; DB 3; 100.0%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CRI-001CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,269
FILING DATE: 13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08558269 Patent No. 5961973
ALIGNALIA MASIA DA RESISTRATION NUMBER: 27,043
REGISTRATION NUMBER: 190.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-574-300
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 376 amino acids amino acids
                                                                                                                                                                                                                                         LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-338-368-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-558-269-10
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Best Local Similarity
Matches 10; Conserve
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237 CEGDSGGPFV 246
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CITY: Bost STATE: MA

COUNTRY:

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RESULT 6 US-08-558-269-10

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100.0%; Score 59; DB 2; Length 579; 100.0%; Pred. No. 0.081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09117708
Patent No. 6060300
GENERAL INFORMATION:
APPLICANT: RADITSHC, Martin; FRIEDRICH, Thomas;
APPLICANT: HOLESCHWEILER, Claus; SCHMIDT, Martin;
APPLICANT: HOEFFKEN, Hans Wolfgang; SCHWEDEN, Juergen;
APPLICANT: and RUEBSAMEN, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Prothrombin Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Prothrombin Light Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombin muteins as antidote for thrombin inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM AT-compatible, Pentium processor OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect version 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/117,708 FILING DATE: 04-30G-1998 CLASSIFICATION: 4.24
                                                   CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LEMCTH: 579 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                  US/08/955,471
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SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
         CURRENT APPLICATION DATA APPLICATION NUMBER: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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TITLE OF INVENTION: th
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Region
LOCATION: 321..579
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region
LOCATION: 1.320
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 CEGDSGGPFV 530
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-117-708-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Prothrombin Light Chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Prothrombin Heavy Chain'
                                                                                                                                 SOFTWARE PATENTING STATES.

SOFTWARE PATENTING STATES.

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

ELING DATE: 22-40G-1994

CLASSIFICATION 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 0S 07/793,989

FILING DATE: 18-NOV-1991

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: FILLING, Thomas

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 10FORMATION:

TELECOMMUNICATION 10FORMATION:
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Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 59; DB 1; Best Local Similarity 100.0%; Pred. No. 0.081; Matches 10; Conservative 0; Mismatches 0
                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08955471
Patent No. 5968751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 John H.
Rolf M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 579 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SET TITLE OF INVENTION: Ant TITLE OF INVENTION: for NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESSE: Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Region
LOCATION: 321..579
OTHER INFORMATION:
US-08-295-411-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.320
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Griffin,
APPLICANT: Mesters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521 CEGDSGGPFV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-955-471-4
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Gaps

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                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A
FILING DATE: 19921230
CLASSIFICATION TAA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING APPLICATION DATE:
PRIOR APPLICATION DATE: 31-MAR-1992
PRIOR APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARTHELES: Steven W
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REFERENCE/COCKET UNMBER: 31,990
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08463953
Patent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                          Sequence 3, Application US/07998972A
Sequence 3, Application US/07998972A
Patent No. 5476777
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor CITY: San Francisco STATE: CA
Pred. No. 0.081;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 1;
Pred. No. 0.086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.08;
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LENGTH: 615 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-07-998-972A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557 CEGDSGGPFV 566
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Best Local Similarity
Matches 10; Conserv
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                                                                                                    521 CEGDSGGPFV 530
                                                              1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-463-953-3
                                                                                                                                                                                    US-07-998-972A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                 RESULT 12
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                                     Length 579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Prothrombin Heavy Chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                     100.0%; Score 59; DB 3; 100.0%; Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCR0472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        PCT-0592-10242-4.
; Sequence 4, Application PC/TUS9210242; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Serine
TITLE OF INVENTION: for Inh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 579 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                     MOLECULE TYPE: protein
; ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-117-708-14
                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : NAME/KEY: Region
: LOCATION: 321..579
: OTHER INFORMATION:
pcr-US92-10242-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region
                                                  linear
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                                                        ropology:
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Gaps

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Length 579;

DB 5;

100.0%; Score 59;

Query Match

CORRESPONDENCE ADDRESS:

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Length 615;
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APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
AURINI APPLICATION DATA:
AURINIALICATION UNMER: PCT/US92/11357
FILING DATE: 1992130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                            FILING DATE: 30-DEC-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
ANDR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/POCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTONNEY/AGENT INFORMATION:
NAME: PARMELE, Steven W
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 13952-12-2
           US 07/998,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9211357 GENERAL INFORMATION:
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100.0%;
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    615 amino acids
amino acid
    DGY: linear

                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 10, Conservative
                                                                                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                             . TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-261-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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557 CEGDSGGPFV 566
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PCT-US92-11357-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
APPLICANT: FOSTEr, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/463,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/462,261
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATMELES, Steven W
REGISTRATION NUMBER: 31,990
REFRENCE/DOCKET NUMBER: 1395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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557 CEGDSGGPFV 566
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                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                               94105
                                                                                                          COUNTRY:
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STATE:
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; TYPE: AMINO ACID ; TOPOLOGY: linear ; MOLECULE TYPE: protein PCT-US92-11357-3

0; Gaps Query Match 100.0%; Score 59; DB 5; Length 615; Best Local Similarity 100.0%; Pred. No. 0.086; Matches 10; Conservative 0; Mismatches 0, Indels (

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1 CEGDSGGPFV 10 ||||||||||| 557 CEGDSGGPFV 566

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Search completed: May 12, 2003, 15:40:35 Job time : 10.6 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:

May 12, 2003, 15:33:02 ; Search time 11.4 Seconds (without alignments) 84.328 Million cell updates/sec

US-09-909-348-1 59 1 CEGDSGGPFV 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	_	_	_	<u> </u>	thrombin (EC 3.4.2	΄.	~	~	thrombin (EC 3.4.2	_	thrombin (EC 3.4.2	hepsin (EC 3.4.21.	polyprotein - Afri	u) Ø		protein C (activat		cal			coagulation factor	hypodermin C (EC 3	serine proteinase	chymotrypsin-like	chymotrypsin (EC 3		11ke		trypsin-like prote
ΩI	F42696	D42696	E42696	H42696	C42696	142696	G42696	S10511	A35827	TBHU	TBBO	S00845	T30337	S45356 .	KXBO	KXHU	849323	T15451	146712	184621	JQ0419	A27802	PS0049	A23473	KYVH2C	S68702	TRWVSY	TRWV3Y	S65465
DB	7	~	~	~	~	7	7	~	?	ч	-	٦	~	7	-	Н	7	7	~	7	~	N	7	~	-	7	-	-	~
% Query Match Length	234	235	235	235	236	236	239	617	618	622	625	417	1524	225	456	461	248	265	275	282	459	230	61	126	218	237	238	254	254
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.9	94.9	89.8	89.8	6	æ	8	88.1	88.1	88.1	86.4	84.7	84.7	84.7	84.7	84.7	84.7	84.7
Score	59	29	59	29	29	29	59	59	59	59	59	26	26	53	53	53	52	52	52	52	52	51	20	20	20	20	20	20	20
Result No.	-	N	m	4	Ŋ	φ	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

1 CEGDSGGPFV 10

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69	28 0 6 4 28 0 6 4	339 07 07	05 63 63
TRFF 1565 1381	\$32794 \$40006 \$56160 \$41308	84724 8353 0C41 8400	S400 A358 B358 C358
466	99999	10000	0000
256 260 264	264 267 270 271	272 472 472	275 275 275 275
84.7 84.7 84.7	84.7 84.7 84.7 7.7	84.7 84.7 84.7	84.7 84.7 84.7
5000 0000	00000	0000 0000	0 0 0 0 0
30 31:		338 40 410	444 544 54

ALIGNMENTS

RESULT 1 F42696 thrombin (EC 3.4.21.5) B chain - Cynops pyrogastor (fire-bellied newt) (fragment) C; Species: Cynops pyrogastor (fire-bellied newt) C; Species: L9-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999	C;Accession: F4209 R;Banfield, D.K.; MacGillivray, R.T.A. Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Reference number: A42696; MUID:92212913; PMID:1557383	Alaces: Sequence not. Alacesion: F42696 Alaceston: F42696 Alaceston: F42696 Alaceston: Preliminary: nucleic acid sequence not shown; not compared with conceptual Alacestone: preliminary: nucleic acid sequence not shown; not compared with conceptual Alacestones: 1-234 CBAN> Alacestones: 1-234 CBAN> Alacestones: 1-234 CBAN> C;Superfamily: thrombin: Gla domain homology; kringle homology; trypsin homology C;Keywords: hydrolase; serine proteinase	Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 234; Best Local Similarity 100.0%; Pred. No. 0.0092; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 CEGDSGGPFV 10 Db 176 CEGDSGGPFV 185	RESULT 2 D42696 thrombin (EC 3.4.21.5) B chain - chicken (fragment) C;Species: Gallus gallus (chicken) C;Species: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999 C;Accession: D42696	R;Banfield, D.K.; MacGillivray, R.T.A. Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Reference number: A42696; MUID:92212913; PMID:1557383 A;Accession: D42696	A:Status: preliminary A:Molecule type: mRNA A;Residues: 1-235 <bana (fragment)="" 1-235="" <bana="" <trx="" a;cross-references:="" a;residues:="" c;reywords:="" c;superfamily:="" domain="" domain:="" f;1-226="" gb:mb1391="" gla="" homology="" homology;="" hydrolase;="" kringle="" proteinase="" serine="" thrombin;="" trypsin=""></bana>	Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 235; Best Local Similarity 100.0%; Pred. No. 0.0093; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Gaps

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thrombin (EC 3.4.21.5) B chain - rainbow trout (fragment)

(Species: Oscorbynchus mykiss (rainbow trout)

(Species: Oscorbynchus mykiss)

(Species: Oscorbynchus mykis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Eptatretus stouti (Pacific hagish)
C; Species: Eptatretus stouti (Pacific hagish)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C; Areasaion: 142696
B; Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. 0:3A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A; Reference number: A42696; MUID:92212913; PMID:1557383
A; Accession: 142696
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Note: nucleotide translation not given
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Superfamily: thrombin; Gla domain homology; Kringle homology (FREYMORD)
                                                                         C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Keywords: hydrolase; serine proteinase F;1-227/Domain: trypsin homology (fragment) <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 236;
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Best Local Similarity 100.
Matches 10; Conservative
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                                        A; Cross-references: GB: M81396
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R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sec A;Reference number: A42696; MUID:92212913; PMID:1557383
                                                                                                                                                                                                                                                                                                                                       R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A;Reference number: A42696; MUID:92212913; PMID:1557383
A;Accession: E42696
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A;Molecule type: mRNA
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: C42696 MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and shacession: C42696; MUID:92212913; PMID:1557383
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C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Reywords: hydrolase; serine proteinase
F;1-226/Domain: trypsin homology (fragment) <TRY>
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C,Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-226/Domain: trypsin homology (fragment) <TRY>
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C;Species: Gekko gecko (tokay)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: E42696
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C;Species: Acipenser transmontanus (white sturgeon)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: H42696
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100.0%; Pred. No. 0.0093;
Live 0; Mismatches 0;
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100.0%; Pred. No. 0.0093;
ive 0; Mismatches 0;
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Best Local Similarity 100.(
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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177 CEGDSGGPFV 186
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A; Residues: 1-235 <BAN>
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Gaps

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A; Molecule type: protein
A; Residues: 44-118, 'N',120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-3
R; Butkowski, R.J.; Ellon, J.; Downing, M.R.; Mann, K.G.
J. Blol. Chem. 252, 4942-4957, 1977
A; Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A; Reference number: A37550; MOID:77207112; PMID:873923
A; Accession: A37550
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A; Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 4
B; Rabiach, M.J.; Blashlil, A; Furie, B.C.
J. Biol. Chem. 261, 13210-13215, 1986
A; Reference number: A37551; MUID:87008532; PMID:3759958
A; Contents: annotation; activation cleavages
R; MacGillivray, R.T.; Irwin, D.M.; Gilnto, E.R.; Stone, J.C.
Ann. N. Y. Acad. Sci. 485, 73-79, 1986
                                                                            A, Molecule Fype: mRNA
A, Residues: 384-618, FZ. CBAN>
A, Residues: 384-618, FZ. CBAN>
A, Residues: 384-618, FZ. CBAN>
A, Residues: 384-618, FZ. CBANB1394
A, Cross-references: GB:M81394
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Reywords: blood coagulation; calclum binding; carboxyglutamic acid; glycoprotein; h. 124-619. Comain: signal sequence #status predicted <PRO>
F; 28-88, Domain: propeptide #status predicted <PRO>
F; 28-88, Domain: gla domain homology <GLA>
F; 28-88, Domain: kringle homology <RRI>
F; 109-187, Domain: kringle homology <RRI>
F; 315-510, Domain: trypsin homology <RRI>
F; 350-51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxyglutamic acid (Glu) #stat F; 61, 91-104, 109-187, 130-170, 158-182, 215-293, 236-276, 264-288, 333-479, 388-404, 533-54
F; 403, 459, 565/Active site: His, Asp, Ser #status predicted
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A; Readdues: 1-622 < DBG>
A; Readdues: 1-622 < DBG>
A; Readdues: 1-622 < DBG>
A; Cross-references: GB: M17262; GB: M33691; NID: 9558069; PIDN: AAC63054.1; PID: 9339641
A; Cross-references: GB: M17262; GB: M3691; N.T.A.; Davie, E.W.
B; Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
B; Deckenistry 22, 2087-2097, 1983
A; Tille: Characterization of the complementary deoxyribonucleic acid and gene coding A; Reference number: A00914; MUID: 83231469; PMID: 6305407
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A;Reaidues: 8-163,'N',165-622 <DE2>
A;Cross-references: GB:V00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344
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N;Alternate names: coagulation factor II
N;Contains: prothrombin
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 30-Nov-1980 f*sequence_revision 22-Jul-1994 f*text_change 08-Dec-2000
C;Accession: A29351; A09914; B00914; A37549; A37550; I51952
A;Title: Nucleotide sequence of the gene for human prothrombin.
A;Reference number: A29351; MUID:88077877; PMID:2825773
A;Reference number: A29351.
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A; Residues: 188-311 <DE3>
R; Walz. D.A.; Hewett-Emmett, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A; Reference number: A37549; MUID:77193964; PMID:266717
A; Accession: A37549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 59; DB 2; 100.0%; Pred. No. 0.023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CEGDSGGPFV 10
A;Accession: A42696
A;Status: preliminary
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A; Cross-references: GB:X55308; NID:953813; PIDN:CAA36548.1; PID:953814
A; Cross-references: GB:X55308; NID:953813; PIDN:CAA36548.1; PID:953814
A; Cross-references: GB:X55308; NID:9782/6
A; Note: the data were obtained from females resulting from the cross of M. domesticus and R; Banfield, D.K.; MacGillivray, R.T.A.
R; Banfield, D.K.; MacGillivray, R.T.A.
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A; Reference number: A42696; MUID:92212913; PMID:1557383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 44-58 < MENN
A; Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
R; Banfield, D.K.; MacGillivray, R.T.A.
Broc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A; Reference number: A42696; MUID:92212913; PMID:1557383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology Reywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr 1-24/Domain: signal sequence *status predicted <SIG>
25-43/Domain: propeptide *status predicted <PRO>
28-88/Domain: gla domain homology <GLA>
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F;109-187/Domain: kringle homology <RR1>
F;215-292/Domain: kringle homology <RR2>
F;360-609/Domain: trypale homology <RR2>
F;505.11,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,F;402,458,564/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
A;Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
B;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A;Title: Profuncional levels are increased in the estrogen-treated immature rat uterus. A;Reference number: A60576; MuID:90091942; PMID:2293980
A;Accession: A60576
                                                               C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Accession: S10511; A60576; B42696
R; Dihanich, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A; Title: cDNA sequence of rat prothrombin.
A; Title: cDNA sequence of rat prothrombin.
A; Reference number: S10511; MUID:90332426; PMID:2377469
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Molecule type: mRNA
Residues: 383-617, E' <BAN>
Cross-references: GB:M81397
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560 CEGDSGGPFV 569
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Best Local Similarity
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A; Residues: 1-617 <DIH>
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A; Status: preliminary
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AMAG

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C;Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothromb c;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb cicomment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb ent interaction with the negatively charged phospholiphid membrane surface.
C;Comment: The prothrombin precursor is synchesized in the liver.
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; gl;F;1-24/Domain: signal sequence #status predicted <PRO>
F;28-84/Domain: ada domain homology (Glab)
F;38-84/Domain: activation peptide 1 #status experimental <FRI>F;109-187/Domain: kringle homology <KR2>
F;214-292/Domain: kringle homology <KR2>
F;214-292/Domain: kringle homology <KR2>
F;214-292/Domain: tringle homology <KR2>
F;216-26/Product: thrombin light chain #status experimental <KR>
F;367-616/Domain: trypsin homology <RRY>
F;367-616/Domain: trypsin homology <RRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Title: Three-dimensional structure of the kringle sequence: structure of prothrombi A; Reference number: A37553; WUID:86296631; PMID:3741841
A; Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
A; Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
Biochemistry 24, 6654-6661, 1985
A; Title: Characterization of the bovine prothrombin gene.
A; Reference number: A3754; WUID:86077733; PMID:3000440
A; Reference number: A3754; WID:86077733; PMID:3000440
A; Contents: annotation; gene structure, T.; Woo, S.L.; Davie, E.W.
Broc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A; Title: Clouing and analysis of a CDNA coding for bovine prothrombin.
A; Reference number: 146045; WUID:81054926; PMID:6254059
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A; Residues: 466-599, Nr., 601-625 cwa2>
A; Cross-references: EMBL: V00135; NID: 9772; PIDN: CAA23451.1; PID: 9808945
B; Pejler, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Biochem. 227, 102-107, 1995
A; Title: Identification of the proteolytic thrombin fragments formed after cleavage w A; Reference number: 867518; MUID: 95154277; PMID: 7851376
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F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;51-66,91-104,109-187,130-170,158-182,214-292,235-275,263-287,339-485,394-410,539-55
F;120,144,419/Msinding site: carbohydrate (Asn) (covalent) #status experimental
F;409,465,571/Active site: His, Asp, Ser #status experimental
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A;Molccule type: protein
A;Molccule type: protein
A;Residues: 318-325;333-338,'X',340;367-374;481-484,'X',486-488;515-522 <PEJ>
C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fi
C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi
tivation peptide and cleaves the remaining part into light and heavy chains. The acti
           Prothrombin and Related Coaquiation Factors, Hemker, H.C.,
                                                     A; Reference number: A37552
A; Accession: A37552
A; Molecule type: protein
A; Reaidues: 44-287, N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625
A; Note: the evidence for 231-Ser is strong
A; Note: disulfide bonds and carbohydrate binding sites were determined
B; Park, C. H.; Tulinsky, A.
Biochemistry 25, 3977-3982, 1986
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$00845

Popsin (EC 3.4.21..) - human

C;Species: Homo sapiens (man)
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Matches 10; Conserv
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A introns: 27/1; 80/3; 89/1; 106/1; 41/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552

C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C; Reywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli

C; Reywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli

C; Reywords: acute phase; blood coagulation; calcium predicted <RGO>

F; 25-43/Domain: signal sequence #status predicted <RGO>

F; 28 87/Domain: propeptide #status experimental <AMT>

F; 44-32/Domain: acityration peptide #status experimental <AMT>

F; 108-186/Domain: kringle homology <KRZ>

F; 21-291/Domain: kringle homology <KRZ>
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F;364-622/Product: thrombin heavy chain #status experimental <RCH>
F;364-622/Product: thrombin heavy chain #status experimental <RCH>
F;364-623/Domain: trypsin homology <TRY>
F;364-65,30.57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status F;60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status F;121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336-550,564-594/Disulfide bonds: #status predicted
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R;MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A;Title: Characterization of bovine prothrombin mRNA and its translation product.
A;Reference number: A00915; MUID:84203525; PMID:6326805
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C; Date: 24-Apr-1984 *sequence_revision 14-U1-1994 *text_change 18-Jun-1999
C; Accession: S02534 *sequence_revision 14-01-1999
C; Accession: S02531; A37552; I46045; S67518
R; Irwin, D.M.; Robertson, R.A.; MacGillivray, R.T.A.
J. Mol. Biol. 200, 31-45, 1988
A; Title: Structure and evolution of the bovine prothrombin gene.
A; Reference number: S02537; MUID: 88245190; PMID: 3379642
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Title: Recombinant genetic approaches to functional mapping of thrombin. Reference number: 151952; MUID:87182874; PMID:3471151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.407/Disulfide bonds: #status experimental
5,462/Active site: His, Asp #status predicted
5/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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R;Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GDB:119894; OMIM:176930
                                                                                                                                             Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A: Residues: 1-230, 'H', 232-625 <MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombin (EC 3.4.21.5) precursor
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Best Local Similarity
Matches 10; Conserv
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Gaps

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C; Superfamily: trypsin; trypsin homology C; Keywords: hydrolase; serine proteinase
                                                                                     89.8%;
90.0%;
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A, Residues: 40-194 <FER>
A, Note: 82-Lys was also found
                                                                                        Query Match 89.8
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                    174 CEGDSGGPLV 183
                                                                                                                                                                                                    1 CEGDSGGPFV 10
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submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from X6
A;Reference number: 220829
                                                             R.Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachl, K.; Davie, E.W.
Blochemistry 27, 1067-1074, 1988
A.Jitle: A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom A.Reference number: $00845; WUID:88209431; PMID:2835076
A.A.Reference number: $00845
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A; Cross_references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Jaccession: S43356
R; Dihanich, M.; Spiess, M.
Biochim. Biophys. Acta 1218, 225-228, 1994
A; Title: A novel serine proteinase-like sequence from human brain.
A; Reference number: S45356; MUID: 94289486; PMID: 8018728
A; Accession: S45356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Xenopus laevis (African clawed frog)
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
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A;Experimental source: Alzhelmer's disease patient brain cortex
C;Genetics:
           31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                          A;MOlecule type: mRNA
A;Residues: 1-417 <LEY>
A;Cross-references: EMBL:X07732; NID:932063; PIDN:CAA30558.1; PID:932064
                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane protein
                                                                                                                                                                                                                                                                                                                    A;Gene: GDB: HPN; TWPRSS1; hepsin
A;Gene: GDB: 135685; OMIM: 142440
A;Gene: GDB: 135685; OMIM: 142440
A;Gene: GDB: 119413: 1
C;Superfamily: hepsin; trypsin homology
C;Superfamily: hepsin; trypsin homology
C;Reywords: hydrolase; liver; serine proteinase; transmembrane protein
F;23-45/Domain: transmembrane #status predicted <TMN>
F;163-400/Domain: trypsin homology <TRX>
F;188-204, 221-359, 322-338, 349-38L/Disnifide bonds: #status predicted
F;203, 257, 353/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%; Score 56; DB 1; Length 417; 90.0%; Pred. No. 0.052; ive 1; Mismatches 0; Indels
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Pred. No. 0.18;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
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Best Local Similarity 90.0%;
Matches 9; Conservative
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243 CQGDSGGPFV 252
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A; Residues: 1-225 <DIH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CEGDSGGPFV 10
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Matches 9; Conserv
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Comment: The gamma-carboxygluteanic acid residues arise by a posttranslational, vita superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol; Reywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind; 1-29, Domain: signal sequence (fragment) *status predicted <SIG> 24-83, Domain: Gla domain homology <CLA> 30-39, Domain: propeptide *status predicted <PRO> 30-39, Domain: protein C light chain *status experimental <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: protein | Residues: 197-454, PV' <STE> | Sessidues: 197-4553, 1983 | Step | Step
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Filtle: Structural changes required for activation of protein C are induced by Ca2+; Reference number: A37542; MUD:83213514; PMID:6406503
Contents: annotation; activation; calcium binding
Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N.Alternate names: autoprothrombin IIA; plasma protein C
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18385; A18386; A00928
R;Long, G.L.; Balagaje, R.M.; MacGilluvray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A;Title: Cloning and sequence of liver CDNA coding for bovine protein C.
A;Reference number: A26250; MUID:85014826; PMID:6091100
                                                                                                                                                       Gaps
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A; Residues: 1-456 <LON>
R; Fernlund, P.; Stenflo, J.
J. Blol. Chem. 257, 12170-12179, 1982
A; Title: Amino acid sequence of the light chain of bowine protein C.
A; Reference number: A18385; MUID:83007325; PMID:6896876
A; Accession: A18385
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A; Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C. A; Reference number: A19316; MUID:83169769; PMID:6572939
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Stenflo, J.; Fernlund, P.
Balol. Cham. 257, 12180-12190, 1982
Filtle: Amino acid sequence of the heavy chain of bovine protein C.
Reference number: A18386; MUID:83007326; PMID:6896877
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F:197-456/Product: protein C heavy chain #status experimental <1
F:197-210/Domain: activation peptide #status experimental <APT>
Length 225;
               DB 2;
                                                                                   0.095
       Score 53; DB 2
Pred. No. 0.095
0; Mismatches
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F;211-440/Domain: trypsin homology <TRX>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #state F;10/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #state F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted F;252,298,397/Active site: His, Asp, Ser #status predicted F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Gaps ö Query Match

89.8%; Score 53; DB 1; Length 456;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 1; Indels

Search completed: May 12, 2003, 15:39:40 Job time : 12.4 secs

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Sequence 4 Sequence 5 Sequence 6 Sequence Sequence

Sequence 4, App Sequence 2, App Sequence 163, Sequence 163, Sequence 163, Sequence 19, App Sequence 31, App Sequence 31, Appendence 31, Appendence 31, Appendence 32, Appendence 33, Appendence 34, Appen

Sequence 247, Sequence 19

OM protein

Run on:

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APPLICANT: Craney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Simmons, David J.
APPLICANT: Samons, David J.
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TITLE OF INVENTION: BEPTIDE DERIVATIVES
FILE REFERENCE: 3033.1002-004
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR APPLICATION NUMBER: 00/-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
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US-09-826-290-247
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10050692 Publication No. US20020182205A1 GENERAL INFORMATION:
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Best Local Similarity
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RESULT 2
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                                                                                                                                                                            May 12, 2003, 15:38:52; Search time 19.4 Seconds (without alignments) 47.436 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
                          GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-050-611-3
US-10-050-611-4
US-10-050-688-5
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 2000000000
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Publication No. US20020187933A1

GENERAL INFORMATION:
APPLICAMT: Carney, Darrell H.
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 3033.1000-008
CURRENT APPLICATION NUMBER: US/10/050,611
CURRENT PILING DATE: 2002-01-16
PRIOR PELING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
                                                                                          APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
TITLE OF INVENTION: Peptide Derivatives
FILE REFERENCE: 3033.1002-001
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Patent No. US20020061852A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
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100.0%; Pred. No. 0.002;
ive 0; Mismatches 0;
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Pred. No. 0.0024;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 12
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Patent No. US20020042373A1

Patent No. US20020042373A1

Patent No. US20020042373A1

Patent No. US20020042373A1

APPLICANT: Carney, Darrell H.

APPLICANT: Crowther, Roger S.

APPLICANT: Stienberg, Janet

APPLICANT: Bergmann, John

TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists

APPLICANT: Bergmann, John

TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists

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TITLE OF INVENTION OF THE OF T
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                                                   APPLICANT: Stiernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: STIMULATION OF CARTILLAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT FILING DATE: 2002-01-16
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100.0%; Pred. No. 0.002;
ive 0; Mismatches 0;
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CTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-1
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PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 6
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 10
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Darrell H.
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-909-122-1
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OTHER INFORMATION: c:terminal amidated fragment of human thrombin FEATURE:
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 3033.1000-008
CURRENT APPLICATION NUMBER: 08/10/050,611
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 50001-07-12
PRIOR PELICATION NUMBER: 60/217,583
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED IITLE OF INVENTION: PEPTIDES
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Pred. No. 0.0044;
; Mismatches 0;
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; OTHER INFORMATION: valine is amidated as CONH2
US-10-050-611-4
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                                        FILE REFERENCE: 3033.1000-008
CURRENT APPLICATION NUMBER: US/10/050,611
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 23
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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US-10-050-611-4
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APPLICANT: Crowther, Roger S.
APPLICANT: Simons, David J.
APPLICANT: Simons, David J.
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: STIMULATION OF BORICANT OF STILLE OF INVENTION: STIMULATION OF BORICANTON WINDER: 09/909,122
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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; LOCATION: (23)...(23)
; OTHER INFORMATION: Valine is amidated as CONH2
US-10-050-692-6
  FILE REFERENCE: 3033.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 12
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Best Local Similarity 100.0%;
Matches 10; Conservative (
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TITLE OF INVENTION: STAULATION OF CARTILAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 3033.1003-004
CURRENT PAPLICATION NUMBER: US/10/050,688
CURRENT PILING DATE: 2002-01-16
PRIOR PPLICATION NUMBER: 60/219,800
PRIOR APPLICATION NUMBER: 60/219,800
RPRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTHARE: FASTENG OF Windows Version 4.0
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APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR APPLICATION NUMBER: 60/209,348
PRIOR PLILING DATE: 2001-07-119
PRIOR FILING DATE: 2000-07-20
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100.0%; Pred. No. 0.0044; '
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100.0%; Pred. No. 0.0044;
iive 0; Mismatches 0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 23
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.

Matches 10; Conservative
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; OTHER INFORMATION: CONH2
US-10-050-688-6
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SEQ ID NO 5
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Patent No. US20020032314A1
GENERAL INCRAMION:
APPLICANT: CAREY, DARELL H.
APPLICANT: RAMARRISHNAN, SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHEP:002
CURRENT APPLICATION NUMBER: US/09/777,328
CURRENT FILING DATE: 1001-02-05
PRIOR PILING DATE: 1994-10-28
NUMBER OF SEQ ID NOS: 94
SECTIORS: PATENTION NOS: 94
SEQ ID NOS: 94
SEQ ID NOS: 94
LENGTH: 23
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- O'THER INFORMATION: Polypeptide, fragment of thrombin US-09-904-091-3
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Sequence 8, Application US/09777328 Patent No. US20020032314A1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Carney, Darrell H.
APPLICANT: Carney, Darrell H.
APPLICANT: Carney, Darrell H.
APPLICANT: Carney, Janet
APPLICANT: Sternberg, Janet
TITLE OF INVENTION: Of The No. US20020042373Al-Proteolytically Activated Thrombin Re
FILE REFERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,800
RICH APPLICATION NUMBER: US 60/219,800
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES
TITLE OF INVENTION: PEPTIDE DERIVATIVES
CURRENT PAPLICATION NUMBER: US/10/050,692
CURRENT APPLICATION NUMBER: US/10/050,692
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR PILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 25

LENGTH: 25
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100.0%; Score 59; DB 10;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 59; DB 9; Best Local Similarity 100.0%; Pred. No. 0.0048; Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
COTHER INFORMATION: fragment of human prothrombin
US-10-050-692-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Peptide fragment of Thrombin US-09-909-348-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-348-5
Sequence 5, Application US/09909348
Patent No. US2002042373A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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LENGTH: 25
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Search completed: May 12, 2003, 15:59:08 Job time: 21.4 secs

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May 12, 2003, 15:31:22; Search time 28.6 Seconds (without alignments)
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
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	(*Tunour arrynments) 46.591 Million cell updates/sec
Title:	US-09-909-348-1
Periect score: Sequence:	osy 1 CEGDSGGPFV 10
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters:	908470
Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Serine esterase co	Serine esterase co	Serine esterase co	Cell growth/adhesi	Nerve tissue regen	Human thrombin rec	Human thrombin hig	Human thrombin pep	Thrombin peptide d	Thrombin-derived p
SUMMARIES	GI	AAE20155	AAU78372	AAM50857	AAW83414	AAB12893	AAB70363	AAE22563	AAE20159	AAU78376	AAM50858
	DB	23	23	23	70	21	22	23	23	23	23
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4	220011 X
e	ID AAE20155 standard; peptide; 10 AA.
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턴	18-JUN-2002 (first entry)
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回	Serine esterase conserved peptide #1.
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3	Cartilage growth; cartilage repair; arthritic joint; tra
3	non-proteolytically activated thrombin receptor; NPAR; (
17.	thorsom tenjantation coring octorses conserved neutific

chondrocyte; serine esterase conserved peptide. therapy; implantation; WO200207748-A2. Unidentified. 31-JAN-2002.

Carney DH, Crowther RS, Stlernberg J, Bergmann J; (TEXA) UNIV TEXAS SYSTEM. WPI; 2002-268953/31.

19-JUL-2001; 2001WO-US22668. 20-JUL-2000; 2000US-219800P. Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteclytically activated thrombin receptor

10 AA;

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine esterase; osteopathic; thrombin; receptor; agonist; bone growth stimulation; osteoinduction; farm animal; companion animal; laboratory animal; bone graft; segmental bone gap; bone void; non-union fracture.
                                The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (MRAR). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is serine esterase conserved peptide. This sequence—is present in the thrombin peptide derivatives which serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stimulating bone growth at a site in a subject in need of osteoliduction, such as a site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated thrombin receptor
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                                                                                                                                                                                                           DB 23; Length 10;
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100.0%; Pred. No. 0.081;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine esterase conserved sequence #1.
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                                                                                                                                                                                                                                                                                                                                                       AAU78372 standard; Peptide; 10 AA.
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            Claim 7; Page 24; 28pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activated thrombin receptor
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Best Local Similarity 100.
Matches 10, Conservative
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                                                                                                                                                         as a NPAR agonist
                                                                                                                                                                               10 AA;
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AAU78372
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present peptide comprises a thrombin-derived serine esterase conserved sequence that is used in a claimed method for promoting cardiac tissue repair. The method involves administering an angiogenic thrombin-derived peptide, especially a thrombin receptor binding domain comprising the 4-amino acid peptide given in AANSOBS6 together with the serine esterase conserved sequence, or preferably the peptide given in AAMSOBS8, which includes both these peptide sequences. The thrombin-derived peptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   these peptide sequences. The thrombin-derived peptide is administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. It is used in claimed methods of stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine esterase; thrombin; revascularisation; vascular occlusion; tissue repair; vulnerary; vasotropic; cardiant; angiogenesis; restenosis; therapy; enzyme; human.
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                                                       Mismatches.
     Score 59;
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Best Local Similarity
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Query Match
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RESULT 4 AAW83414 Synthetic

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contains a peptide immobilised to a base which consists of a contains a peptide immobilised to a base which consists of a bylogaccharide gel such as alginic acid. Sequences AABI2886-B12899 represent examples of the peptides used in the nerve regeneration material. The peptide containing material causes nerve cell repositions and also causes axonal extension. The material can be used for the treatment of central or peripheral nervous system disorders, spinal disorders, head injury or cerebrovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic neutrophil cell chemotactic peptides, useful for generating antibodies for modulating neutrophil chemotaxis in immune response and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neutrophil cell chemotactic; wound healing; inflammation; vulnerary; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to a new nerve regenerative material which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human thrombin receptor binding domain peptide SEQ ID NO:8.
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100.0%; Pred. No. 0.16;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nerve regeneration material
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                              (KURS ) KURARAY CO LTD. (NISH/) NISHIMURA Y: (SUZU/) SUZUKI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-202003/20.
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                                                                                                                                                                                                                                                                                                                (SUZU/) SUZUKI Y.
(TANI/) TANIHARA M.
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JP2000143531-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6184342-B1.
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                                                                                                                                                                                       09-SEP-1998;
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                                                                                                                         11-AUG-1999;
                                                              23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide or its salt as the active component. The peptide and its salt can be used for covering injuries, promoting adhesion of biotissues, bone reinforcing and nerve regeneration. The present sequence represents a specifically claimed peptide of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a material for medical treatment which comprises one or more peptides of the formula XADEGJIMPTOQY, or their salts, immobilised on a substrate: where X = H, CH3CO or CH3COLys;
A = Ser or Th; D = Ile, Val or Leu; B = Lys or Arg; G = Ile, Val or Leu; J = Gly or Ala; L = Ile, Val or Leu; M = Gly or Ala; D = Gly, Ala or Gly-Lys-Lys-Lys-Gly; T = OH or NH2. Also described is an agent for cell growth promotion and/or cell adhesion promotion containing the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Material for medical treatment comprises new peptide - used for covering injuries, promoting adhesion of bio-tissues, bone
                                                                                                                                                                                                                                                                                                                                                                                 biotissue; bone reinforcement; nerve regeneration; HMP resin
                                                                                                                                                                                                                                                                                                                                                       Cell growth; adhesion; promotion; medical treatment; injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 59; DB 20; Length 23; il Similarity 100.0%; Pred. No. 0.16; 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                            Cell growth/adhesion promoting peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reinforcing and nerve regeneration
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                                                                                                  AAW83414 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 12; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0140885
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                                                                                                                                                                                                                                 26-FEB-1999 (first entry)
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Best Local Similarity
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Synthetic

AAB12893;

Sequence

Matches

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Gaps

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Length, 23; Indels us-09-909-348-1.rag

23 AA;

Sequence

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neutrophil cell chemotactic agent. (I) has vulnerary and antiliflammatory activities. (I) is useful as a potent neutrophil cell chemotactic agent and for generating antibodies against the peptides, which are useful for modulating neutrophil recruitment to a wound site for enhancing or inhibiting inflammation and early effects of wound healing. Neutrophil response to (I) is specific, since monogytes and fibroblasts do not show any expression of the receptor to which (I) binds. The present sequence represents a human thrombin receptor bliding domain peptide which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel synthetic peptides and antibodies which are potent chemotactic agents for neutrophils. The peptides of the invention mimic the activity and role of the cleavage fragment of the proteolytically activated receptor for thrombin (PART). They are useful for stimulating or modulating neutrophil cell chemotactic migration or for generating an antibody. In particular, the peptides of the invention are useful for modulating neutrophil recruitment to a wound site for enhancing or inhibiting inflammation and early effects in wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  They are also useful for modulated neutrophil chemotaxis in immune response. The present sequence is high affinity receptor binding domain of human thrombin. This peptide is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic peptide neutrophil cell chemotactic agents, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; proteolytically activated receptor for thrombin; neutrophil; chemotactic agent; PART; inflammation; wound healing; chemotaxis; immune response; vulnerary; thrombin; receptor binding domain.
                        present invention describes a synthetic peptide (I) which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stimulating or modulating neutrophil cell chemotactic migration, particularly for modulating neutrophil recruitment during immune
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                                                                                                                                                                                                                                                                                 Length 23;
                                                                                                                                                                                                                                                                                 100.0%; Score 59; DB 22; Length 2
100.0%; Pred. No. 0.16;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human thrombin high affinity receptor binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHRY-) CHRYSALIS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE22563 standard; peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 3; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response or in wound healing
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                                                                                                                                                                                                                                                                                                   Local Similarity 100.
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                                                                                                                                                                                                                                         23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteclytically activated thrombin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (NRRN). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NRRR agonist to provide calls for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide derivative which serves
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                Cartilage growth; cartilage repair; arthritic joint; traumatic injumon-proteolytically activated thrombin receptor; NPAR; chondrocyte; therapy; implantation; thrombin peptide; human.
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 Length 23;
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 DB 23;
                   0.16;
                                        Mismatches
   Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stiernberg J,
                                                                                                                                                                                                                                                                                                                Human thrombin peptide derivative #2.
                                                                                                                                                                                                     AAE20159 standard; peptide; 23 AA.
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 100.0%;
100.0%;
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                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carney DH, Crowther RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                        Conservative
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Query Match
Best Local Similarity
Matches 10; Conserv
                                                                        1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as a NPAR agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                           18-JUN-2002
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                                                                                                                                                                                                                                       AAE20159;
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AAU78376
ID AAU7
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AC AAU7
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Tue May 13 09:54:53 2003

(first entry)

18-JUN-2002

Location/Qualifiers

/label- Unknown

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The invention describes a method of stimulating bone growth at a site in a subject in need of osteoladuction. The method involves administering an agonist to stimulate bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoladuction, such as the site in need of a bone graft in a subject, a segmental bone gap, a bone vid or a non-union fracture. This sequence represents a thrombin peptide derivative obtained from a serine esterase that can stimulate or activate the non-proteolytically activated thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stimulating bone growth at a site in a subject in need of osteoinduction, such as a site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 22; 27pp; English
                                                                                                                                                18-JUL-2001; 2001WO-US22641.
                                                                                                                                                                                                                                       19-JUL-2000; 2000US-219300P
                                                                                                                                                                                                                                                                                                                 (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                Crowther RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-303796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombin receptor
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WO200205836-A2
                                                                              24-JAN-2002
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Redin WR;

Yang J,

Simmons DJ,

Gaps . Length 23; Indels ö 100.0%; Score 59; DB 23; 100.0%; Pred. No. 0.16; ive 0; Mismatches 0; Query Match 100.

Best Local Similarity 100.
Matches 10; Conservative å

AAM50858 standard; Peptide; 23 AA. AAM50858; RESULT 10 AAM50858

Thrombin-derived peptide used to promote cardiac tissue repair

01-MAY-2002 (first entry)

Thrombin; revascularisation; vascular occlusion; tissue repair; vulnerary; vasotropic; cardiant; angiogenesis; restenosis; therapy; human.

Homo sapiens

Promoting cardiac tissue repair, stimulating revascularisation, stimulating vascular endothelial cell proliferation, and inhibiting vascular occlusion by using anglogenic thrombin derivative peptide that includes a thrombin receptor binding domain sequence (see als AAM50856) and a serine esterase conserved sequence (see also AAM50857). The peptide is used in a claimed method for promoting cardiac tissue repair. It is administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. The thrombin formulated as a sustained release formulation. The thrombin proliferation, stimulating vascular endothelial cell proliferation, inhibiting vascular endothelial cell restenois following balloon angioplasty, in which case it may be "serine esterase conserved sequence" /note- "thrombin receptor binding domain" 12..23 Location/Qualifiers Claim 4; Page 19; 24pp; English 12-JUL-2001; 2001WO-US21944 12-JUL-2000; 2000US-217583P (TEXA) UNIV TEXAS SYSTEM. coated onto the catheter. 12..23 /note= WPI; 2002-179665/23. 23 AA; WO200204008-A2. Carney DH; Sequence Key Peptide Peptide

Gaps ö DB 23; Length 23; Indels ö Score 59; DB 23 Pred. No. 0.16; Mismatches ö 100.0%; 100.0%; Conservative Query Match Best Local Similarity Matches 10; Conserv

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1 CEGDSGGPFV 10 14 CEGDSGGPFV 23 à 셤

RESULT 11 AAW99113

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AAW99113 standard; protein; 111 AA. Bovine zeta 2 prethrombin 2. 14-MAY-1999 AAW99113;

Prothrombin; exosite assay; anticoagulant; blood clot; thrombin; cardiovascular disease; stroke; haematological disorder. W09855130-A1 10-DEC-1998 Bos sp

98WO-US10840. 98US-0081030. 97US-0048864. 08-APR-1998; 06-JUN-1997; 28-MAY-1998;

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CC an exosite assay has been developed for inhibition of the catalytic cleavage of prothrombin (PTh) to thrombin (Th) by prothrombinase (I), at a site remote from the catalytic site of (I) comprises: (a) preparing a colution containing 0.05-20 mu M substrate (S), that includes a protease cleavage site and exosite-binding determinant; 0.05-200 nM factor Va; 0.50-500 micro M phospholipids (PL); test inhibitor (A) in buffer of pH (CC 79, containing 1-10 mM calcium ions but no calcium-chelating agent; (CC 10) initiating catalytic cleavage of (S) by adding an aliquot of factor Xa (to final concentration 0.05-200 nM) so that there is an excess of va (CC Xa, forming a S(I) complex; (C) withdrawing aliquots of the creation mixture, quenching them; and (d) assaying for concentration of Th. Alternatively, in the initial solution S is replaced by the same concentration of Xa (less than the amount of Va), and reaction is started by adding S. Also described in the present invention are inhibitors (A) having ICSO less than 1 mu M identified by this assay. (A) are potentially useful as a new class of anticoagulants for treatment of cardiovascular disease, stroke and haematological disponders. The method is based on the finding that exosite interactions are critical for represents human zeta. 2 prethrombin 2.

The present sequence of the present sequence of the second parametric of the present sequence of the sequence of the second parametric of the present sequence of the sequence of the second parametric of the sequence of the second parametric of the present sequence of the sequence of the second parametric of the present sequence of the sequence of the second parametric of the present sequence of the sequence of the second parametric of the sequence of the
                                                  Exosite assay for agents that inhibit catalytic cleavage of prothrombin - at sites away from the active site of prothrombinase, also new inhibitors, potentially useful as anticoagulants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutein; platelet aggregation; blood clotting;
decrease; hirudin; heparin; anti-thrombin III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Asp residue has been replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 59; DB 20; Length 116; 100.0%; Pred. No. 0.63; 0; Indels 1.1ve 0; Mismatches 0; Indels
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                                                                                                                                                                        Disclosure; Page 44-45; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW11545 standard; Protein; 259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human thrombin Asn99 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-AT00105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95AT-0001006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coagulation; reduce;
antagonist; D99N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prothrombin; mutant;
WPI; 1999-070237/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEGDSGGPFV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMO ) IMMUNO AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW11545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AAW11545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                                                                                                                                                                   An exosite assay has been developed for inhibition of the catalytic cleavage of prothrombin (PTh) to thrombin (Th) by prothrombinase (I), at a site remote from the catalytic site of (I) comprises: (a) preparing a solution containing 0.05-20 mu M substrate (S), that includes a protease cleavage site and exosite-binding determinant; 0.05-200 mM factor Va; 0.50-50 micro M phospholipids (PL); test inhibitor (A) in buffer of pH (7-9, containing 1-10 mM calcium ions but no calcium-chelating agent; (b) initiating catalytic cleavage of (S) by adding an aliquot of factor Xa (to final concentration 0.05-200 mM) so that there is an excess of Va over Xa, forming a S/(I) complex; (C) withdrawing aliquots of the caection mixture, quenching them; and (d) assaying for concentration of Xa (less than the amount of Va), and reaction is started by adding S. Also described in the present invention are inhibitors (A') having IC50 less than 1 mu M identified by this assay. (A') are concentration described in the present invention are inhibitors (A') having IC50 less than 1 mu M identified by this assay. (A') are cardiovascular disease, stroke and haematological disorders. The method is based on the finding that exosite interactions are critical for concentrate specificity in catalytic formation of Th. The present sequence concentrate specificity in catalytic formation of Th. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                    Exosite assay for agents that inhibit catalytic cleavage of prothrombin - at sites away from the active site of prothrombinase, also new inhibitors, potentially useful as anticoagulants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exosite assay; anticoagulant; blood clot; thrombin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 59; DB 20; Length 111; 100.0%; Pred. No. 0.6; 1.ve 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disease; stroke; haematological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represents bovine zeta 2 prethrombin 2
                                                                                                                                                                                                                                                                                                       Disclosure; Page 42-43; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99115 standard; protein; 116 AA.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                 WPI; 1999-070237/06.
                       (UYEM-) UNIV EMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA;
                                                                            Krishnaswamy S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYEM-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krishnaswamy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prothrombin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09855130-A1
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06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Prothrombin mutants having one or more changes in amino acid sequence compared with the natural protein and having 0.10% (preferably 0.0.25%) of the activity of the natural protein are claimed, provided that changes in amino acid sequence do not affect the capacity of the mutants to bind to specific ligands and receptors. The mutants have greatly reduced clotting activity and are useful as antagonists of thrombin inhibitors such as hirudin, heparin and anti-thrombin III. The mutations may also result in changes to the in vivo half-life of prothrombin. The half-life may be reduced to less than 10 minutes or the mutant prothrombin may have an extended half-life of more than
                                                                                                                                                                                                                                                                                                                        i hour, making it useful as an anticoagulant and to inhibit side-
effects of anti-coagulant treatment. They are converted to inactive
thrombin and are able to compete with native, active thrombin for
binding to receptors. The present sequence represents the thrombin
mutant which is derived by trypsin cleavage of a specifically
claimed human prothrombin mutant in which has at position 419 is
changed to Asn. The thrombin Asn99 mutant was found to have only
0.24% of the activity of wild-type thrombin on a chromogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Note: This sequence does not appear in the specification and has been produced by modifying the wild-type sequence of human prothrombin which appears in figure 1).
                                                                  Prothrombin mutants with reduced clotting activity – useful as antagonists of thrombin inhibitors or for anticoagulant therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 259;
Schlokat U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 59; DB 18;
100.0%; Pred. No. 1.2;
iive 0; Mismatches 0;
 Mitterer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
37. 295
/note= "mature protein"
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                                                                                                                     Example 3; Page -; 73pp; German.
Falkner F, Fischer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0258038
93US-0152657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 CEGDSGGPFV 210
                                  WPI; 1997-065455/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wild-type thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
tes 10; Conserv
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12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        substrate.
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 Eibl J,
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Matches
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The sequence reresents wild-type (reference) thrombin. Mutants of this sequence (AAR74776-80 and AAR76033-41) have at least 80% homology with thrombin, and are capable of protein-c activation without significant fibrinogen clotting activity, and vice versa clotting activity of less than 0.5 or greater than 2 compared to thrombin. The mutant thrombin sequences, produced in recombinant conditions on by in vitro methods, and are used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
                                                                                                Thrombin derivs with segregated pro- and anticoagulant activities useful for treating thrombotic disorders but also diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombin; oligonucleotide-directed mutagenesis; procoagulant; anticoagulant; protein engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 59; DB 16; Length 295; 100.0%; Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Arg in wild-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                     Disclosure; Fig 1; 78pp; English.
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                 Tslang M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0258038
93US-0152657
                                                                                                                                     treatment of tumours, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37..295
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                Leung LLK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111111111
237 CEGDSGGPFV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GILE-) GILEAD SCI.
                                                WPI; 1995-194103/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                             295 AA;
                                                                 N-PSDB; AAQ92455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1994;
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12-NOV-1993;
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                 Gibbs CS,
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Thrombin derivs with segregated pro- and anticoagulant activities

(GILE-) GILEAD SCI.

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Gaps

useful for treating thrombotic disorders but also diagnosis, treatment of tumours, etc.

Claim 22; Page 63/3; 78pp; English.

The mutant thrombin sequence, generated by oligonucleotide-directed mutagenesis, has at least 80% homology with thrombin, and is capable of protein-C activation without significant fibrinogen clotting activity, and vice versa. (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin). The mutant thrombin is produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.

295 AA; Sequence

0; Gaps Query Match 100.0%; Score 59; DB 16; Length 295; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 10; Conservative 0; Mismatches 0; Indels

1 CEGDSGGPFV 10 ð

237 CEGDSGGPFV 246

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Search completed: May 12, 2003, 15:36:02 Job time: 29.6 secs

OM protein

Run on:

Sequence:

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Q9dfdl oncorhynchu
Q91vq8 mus musculu
O45045 scirpophaga
Q924u6 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                    O9v5y4 drosophila
018448 helicoverpa
Q9ylk4 anopheles g
Q9dc82 mus musculu
                                                                                                                                                                                                                                                                                                                                                 09cq78 mus musculu
09nr68 homo sapien
                                                                                                                                                               heliothis z
boltenia vi
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29ttrO canis famil
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                                                                                        drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amplification and sequence analysis of the B chain of thrombin from nine different species."; proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acipenser transmontanus (White sturgeon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
                                                                                      Q9v513
Q8sy35
                                                                                                                                                                                                 027458
017800
09vwd8
                                                                                                                                                                                                                                                       09bpq4
09vzt0
09vh83
                                                                                                                                               0960g6
09nb78
                                                                        09u113
                                                                                                                            09b119
                                                                                                                                                                                    017439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Banfield D.K., MacGillivray R.T.A.;
"Partial characterization of vertebrate prothrombin cDNAs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45C558D6618E0585 CRC64;
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Last annotation update)
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UNKNOWN_1.
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InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01354; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_ESR; 1.
Hydrolase; Serine protease.
NON_TER 1 1
SEQUENCE 234 AA; 26846 MW; 45C558D661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                              09GTK6
09TV90
09C078
09NR68
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Q9DC82
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                                                                                                                                                                                                                    017800
09VWD8
09BPQ4
                                                                                                                                                                                                                                                                              Q9V2T0
Q9VH83
                                                                                                                                               950960
                                                                                                                                                                 09NB78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LIVER;
MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20, Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M81399; AAA48514.1;
HSSP; P00734; 2HNT.
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                                                                        1462
1557
1674
2382
2409
187
245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7904;
   Acipenser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THROMBIN
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Q90244;
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Q90244
   SOLUTION OF THE PROPERTY OF TH
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091218 oncorhynchu
090504 eptatretus
091001 gallus gall
09ptw7 struthio ca
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Q9bk47 luidia foli
Q9cw97 mus musculu
Q91674 xenopus lae
Q9v514 drosophila
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Q90387 cynops pyrr
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096rg0 homo sapien
045029 drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              May 12, 2003, 15:32:37; Search time 22.6 Seconds (without alignments) 91.171 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                          671580
                     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q91001
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Q9BK47
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045029
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Gapop 10.0 , Gapext 0.5
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p_unclassified:*
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sp_bacteriap:*
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seq length: 200000000
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sp_bacteria:*
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59
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Match 1
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Perfect score:
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Minimum DB Maximum DB

Database

8 111 113 114 114 115 115 116 117

Result 잁

Searched:

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Banfield D.K., MacGillivray R.T.A.;
"Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from
nine different species.";
Proc. Natl. Acad. Sci. 0.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cynops pyrrhogaster (Japanese common newt),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea; Salamandridae, Cynops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banfield D.K., MacGillivray R.T.A.;
Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from
nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 235;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 59; DB 13; 100.0%; Pred. No. 0.0098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
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                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; I.
PROSITE; PS50240; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_ERR; I.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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SMART; SM00020; TYP_SPC: 1.
PROSITE; PS60240; TRYPSIN_DOM; 1.
PROSITE; PS60134; TRYPSIN_HTS; UNKN
PROSITE; PS60135; TRYPSIN_SER; 1.
HYdrolage; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92212913; PubMed-1557383;
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EMBL; M81395; AAA49391.1; -.
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                    EMBL; M81392; AAA49309.1; -. HSSP; P00734; 1B7X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ul-NOV-1996 (TrEMBLREL 01,
01-MAR-2002 (TrEMBLREL 20,
Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 CEGDSGGPFV 186
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                                                                                                                                                                                                                                                                                                                  MEROPS; S01.217
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SEQUENCE
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SEQUENCE
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Q90387;
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Q90387
REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amplification and sequence analysis of the B chain of thrombin fronted different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gecko gecko (Tokay gecko).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
NCBI_TaxID-36310;
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                       100.0%; Score 59; DB 13; Length 234; 100.0%; Pred. No. 0.0097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banfield D.K:, MacGillivray R.T.A.;
"Partial characterization of vertebrate prothrombin cDNAs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 235;
                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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100.0%; Pred. No. 0.0098;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          235 AA
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                                                                                0; Mismatches
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00130; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_IPMOTITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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091004;
01-NOV-1996 (TEMBLEEL: 01,
01-NOV-1996 (TEMBLEEL: 01,
01-MAR-2002 (TEMBLEEL: 20,
              Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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THROMBIN.
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                                                                                                                                                                         177 CEGDSGGPFV 186
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                                                                                                                                   1 CEGDSGGPFV 10
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Q28731
ID Q28731
Q28731,
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091004
1D 09100
DT 01-N
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DT 01-N
DE Thrc
GN THRC
GN GECH
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OC LEPI
OC LEPI
OC LEPI
OC NCB:
RN [1]
RP SEQI
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MEDLINE-94223694; PubMed-7513365;
Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.;
"Evolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin.";
J. Mol. Evol. 38:177-187(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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"Partial characterization of vertebrate prothrombin cDNAs:
amplification and sequence analysis of the B chain of thrombin from
nine different species.";
        Banfield D.K., MacGillivray R.T.;
"Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS01040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SSR; 1.
PROSITE; PS00135; TRYPSIN_SSR; 1.
Hydrolase; Serine protease.
SEQUENCE 420 AA; 47888 WW; 64522AA21A57!
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InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
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PRINTS; PRO0018; KRINGLE.
PRODON; PRO00395; Kringle; 1.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M81393; AAA21620.1;
HSSP; P00734; 1UVS.
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les 10; Conserv
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091001;
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Q91001
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                     E REPRESENTATION OF THE PROPERTY OF THE PROPER
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                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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                                                Indels
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                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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. 0.0098;
0;
                                                                                                                                                                                                                                                                               239 AA
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SMART; SMOODO; CHYMOTRYPSIN.

PROSITE; PSOSO40; TRYPSIN.DOM; 1.

PROSITE; PSO3013; TRYPSIN.DOM; 1.

PROSITE; PSO0135; TRYPSIN.LSER; 1.
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                  Pred. No. 0.
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01-NOV-1996 (TIEMBLIEL. 01, Last sequ
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TISSUE-LIVER; — MEDLINE-92212913; PubMed-1557383;
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MEDLINE-92212913; PubMed-1557383;
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                     100.0%;
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HSSP; P00734; 1B7X.
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Matches 10; Conservative
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                                                Conservative
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                  Best Local Similarity
Matches 10; Conserv
                                                                                                1 CEGDSGGPFV 10
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090504;
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EMBL; AB028871; BAA89046.1;
HSSP; P00734; 1UVS.
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hes 10; Conservative
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                                                                                                                                                      PRINTS; PR00018; KRINGLE
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                                                                                                                                                                                                                                                                                                608 AA;
                                                                                                                                                                                                                                                                                                                                                                      1 CEGDSGGPFV 10
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                         MEROPS; S01
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                                                                                                                                                                 ProDom; SMART; SI
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Q9NBC9
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                    MEDLINE-94223694; PubMed-7513365;
Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.;
"Evolution of prothrombin: isolation and characterization of the cDNAs
encoding chicken and hagfish prothrombin.";
J. Mol. Evol. 38:177-187(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.; "Purification and characterization of ostrich prothrombin."; Int. J. Blochem. Cell Biol. 32:1151-1159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Struthio camelus (Ostrich).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . J. Biochem. Cell Biol. 32:1151-1159(2000).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 13; Length 607;
Pred. No. 0.025;
); Mismatches 0; Indels
                                                                                                                          Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; M81391; AAA21619.1; -- HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine protease.
SEGHENCE 607 AA; 69110 MW; 002F3605EA36270F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   608 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                          InterPro; IPR001254; Ser_protease_Try
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                    100020; Tryp_SPc; 1.
PS00011; GLU_CARBOXYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20579470; PubMed-11137455;
                                                                                                                                                                          InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
                                                                                                                                                                                                  Kringle.
Prothrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                  PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                           KRINGLE_1; ;
                                                                                                                                                                                                                                                                                                                  PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                       KRINGLE_2
                                                                                                                                                                                                                                                           Pfam; PF00051; Kringle; 2. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                           PRINTS; PRO0018; KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                 Pfam; PF00594; gla; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 CEGDSGGPFV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8801;
                                                                                                                                                               501.217
                                                                                                                Banfield D.K.;
                                                                                                        LIVER
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                                                                                                                                                                                                  InterPro:
                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                MEROPS;
                                                                                                                                                                                                                                                                                                                                                          SMART;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIANE 21135159; PubMed-11240636;
Yan J., Cheng Q., Li C.B., Aksoy S.;
"Molecular characterization of two serine proteases expressed in gut
tissue of the African trypanosome vector, Glossina morsitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insect Mol. Biol. 10:47-56(2001).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 59; DB 13; Length 608; 100.0%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69392 MW; 11B974B9AEE54EA2 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 21, Last annotation update)
Trypsin-like serine protease precursor.
Glossina morsitans morsitans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0722; CHYMOTREPSIN.
SMART; SM00102); TYPESESPE; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_ERF; 1.
PROFIED; Protesse; Serine protesse; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               SM00020; Tryp_SPc; 1.
5; PS00011; GLU_CARBOXYLATION; 1.
5; PS00021; KRINGLE_1; 2.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002381; GLA_blood.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protesse_Try.
InterPro; IPR000294; VitK_dep_GLA.
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InterPro; IPR001254; Ser_protease_Try
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                                                                                                                                                                                                                                    PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                       ; PD000395; Kringle; 2. SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50070; KRINGLE_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease.
                                                                                                                                         Pfam; PF00594; gla; 1.
Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
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SO

Q9BK47; Q9BK47;

RESULT 10

à g **09BK47**

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PRT; 1524 AA
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SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_SPC; 1.
PROSITE; PS00098; THIOLASE_1; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_DOM; 1.
HYdrolase; Serine protesse.
                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1196620; Hpn.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001190; Srcr_receptor.
InterPro; IPR002155; Thiolase.
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MEDLINE-99432219; PubMed-10500163;
                MEDLINE-21085660; PubMed-11217851;
STRAIN-C57BL/6J; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                       TRYPSIN FAMILY.
EMBL; AK002694; BAB22289.1;
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00089; trypsin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 CQGDSGGPFV 443
                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.224; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
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SEQUENCE
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Matches
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                                                                             Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 262:73-80(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-21100442; PubMed-11179669;
Vickery M.C.L., Vickery M.S., McClintock J.B., Amsler C.D.;
Vickery M.C.L., Vickery M.S., McClintock J.B., Amsler C.D.;
Tutilization of a novel deuterostome model for the study of
regeneration of genetics: Molecular cloning of genes that are
differentially expressed during early stages of larval sea star
regeneration.";
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library,
clone:0610030A17, full insert sequence (Fragment).
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Valvatacea; Paxillosida; Luidiidae; Luidia.
NCBI_TaxID=105861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 5; Length 267;
Pred. No. 0.038;
1; Mismatches 0; Indels
                                                Length 255;
 TRYPSIN-LIKE SERINE PROTEASE. E914E31FB7DD6579 CRC64;
                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Protease; Serine protease.
SEQUENCE 267 AA; 28761 MW; 88F61A061921860C CRC64;
                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sea StAR regeneration-associated protease SRAP.
                                            94.9%; Score 56; DB 5; 90.0%; Pred. No. 0.036; 1ve 1; Mismatches
                                                                                                                                                                                                                     267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00089; trypsin; 1.
PRINTS; PR0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPS; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF312826; AAK15274.1; -. HSSP; P00763; 1DPO.
   255 TI
27565 MW;
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                                           Ouery Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                     PRELIMINARY;
 28 2
255 AA;
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                                                                                                                           1 CEGDSGGPFV 10
                                                                                                           1 CEGDSGGPFV 10
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                               Luidia foliolata.
   CHAIN
SEQUENCE
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Best Loca Matches

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09CM97

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
Ramanaka T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.S., Sizuki R., Tomita M., Wagner L., Washio T.,
Ra Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
Radai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Radustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Ryons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
Ryorone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ryasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Ryasaki W., Salosaki W., Rasegawa Y., Kawaji H., Rohtsuki S.,
Ryasaki V., Wang K.H., Rasegawa Y., Kawaji H., Rohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lindsay L.L., Yang J.C., Hedrick J.L.;
"Ovochymase, a Xenopus laevis egg extracellular protease, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.9%; Score 56; DB 11; Length 502; 90.0%; Pred. No. 0.072; 1ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 AA; 53069 MW; 97BE638938CC4FCC CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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translated as part of an unusual polyprotease.";
Proc. Natl. Acad. Sci. U.S.A. 96:11253-11258(1999).
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EMBL; AE003835; AAF59008.1; -.
HSSP; P00763; 1DPO.
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90.0%;
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EMBL; AF072690; AAC25596.1;
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Burlis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., Charler A., Chandra I., Charley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
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                                                   "CDNA Cloning of Ovochymase, a Chymotrypsin-like Protease Released From Xenopus laevis Eggs at Fertilization.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 4 CUB DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Last sequence update)
Last annotation update)
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00020; Tryp_SPC; 3.
PROSITE; PS01180; CUB; 5.
PROSITE; PS50240, TRYPSIN_DOM; 3.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_3.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_3.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_3.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_3.
                                   ., Lindsay L.L., Hedrick J.L.;
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR001254; Ser_protease_fry.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; CUB; 5. Pfam; PF0089; trypsin; 3. PRINTS; PR00022; CHIMOTRYPSIN. SMART; SM00042; CUB; 4.
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HSSP; P00763; 1DPO.
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Matches 9; Conservative
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1524 AA;
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SEQUENCE FROM N.A.
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Q9V514
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A Barris N.L., Barvey D., Heiman T.J., Wan P., Harris N.,

Rarris N.L., Barvey D., Heiman T.J., Wal M.-H., Ibegwam C.,

A Jali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Radiali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Radiali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Lid Z.,

Radiasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Radiasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Radiasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Radiasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Radiasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Radiasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Radiasko M., Malbhina N.V., Mobarry C., Morris J., Moshrefi A.,

Radiasko M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Radiasko M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Radiasko M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

Radiasko M., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Radiasko M., Pittman G.S., Zhan M., Zhang S., Yao Q.A.,

Radiasko M., Wang R.N., Robing W., Zhou X., Zhu X., Smith H.O.,

Radiasko M., Myers B.W., Rubin G.M., Venter J.C.;

Radiasko M., Myers B.W., Rubin G.M., Venter J.C.;

Radiasko M., Radiasko M., Venter J.C.;

Radiasko M., Polyman R., Rubin G.M., Venter J.C.;

Radiasko M., Radiasko M., Venter J.C.;

Radiasko M., Mars B.W., Rubin G.M., Venter J.C.;

Radiasko M., Mars M
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Eur. J. Biochem. 262:627-65(1999).
-I-.SIMILARITY: BELONGS TO PEPTIDASE PAMILY SI; ALSO KNOWN AS THE
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MEDLINE-99339928; Pubmed-10411621;
Yan X.-H., De Bondt H.L., Powell C.C., Bullock R.C., Borovsky D.;
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Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Peteryota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Curculionidae; Entiminae; Entimini;
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Pred. No. 0.12;
0; Mismatches 1; Indels
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001224; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Hydrolase; Serine protease.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_raxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21226193; PubMed-11327827;
MEDLINE-21226193; PubMed-11327827;
Takayama T.K., Carter C.A., Deng T.;
Takayama T.K., Carter C.A., Deng T.;
TACLIVATION of prostate-specific antigen precursor (pro-PSA) by prostin, a novel human prostatic serine protease identified by prostin, a novel human prostatic serine protease identified by Biochemistry 40:1679-1687(2001).

EMBL. AF303046; AAK62813.1;
InterPro; IPR001254; Ser_protease_Try.
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80.0%; Pred. No. 0.12;
iive 2; Mismatches 0; Indels
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23 252 TRYPSIN.
252 AA; 26064 MW; EE0EDBF116B042AB CRC64;
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1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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PROSITE; PS50240; TRYPSIN, DOM; 1.
Hydrolars; PS00134; TRYPSIN, IIS; UNKNOWN.1.
Hydrolass; Serine protease.
SEQUENCE 255 AA; 27986 WW; 00D5B79E140
                                                             PRINTS; PR00722; CHTMOTRIPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_EBR; 1.
Hydrolase; Serine protease; Signal.
IPR001314; Chymotrypsin.
IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Best Local Similarity 80.0
Matches 8; Conservative
                                                 fam; PF00089; trypsin; 1
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                                                                                                                                                                                                                                            SEQUENCE
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096RQ0;
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1 CEGDSGGPFV 10

õ g Search completed: May 12, 2003, 15:38:38 Job time: 24.6 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:

May 12, 2003, 15:32:07; Search time 5.8 Seconds (without alignments) 71.511 Million cell updates/sec

US-09-909-348-1 59 Title: Perfect score:

1 CEGDSGGPFV 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	18292	_	P00734 homo sapien	5 bos	พกร พ	homo s	canis	capra	felis	-	macac	рошо	Q9ukr3 homo sapien	gog				09pt41 vipera lebe	_		P16294 mus musculu		P35043 lucilia cup	P00769 vespa crabr	P24664 saccharopol	Q9bzj3 homo sapien	P29787 aedes aegyp	Q92876 homo sapien	_	fusar	homod	homo	. Oppoga nomo sapien
SUMMARIES	Œ	THRB_RAT	THRB_MOUSE	THRB_HUMAN	THRB_BOVIN	HEPS_MOUSE	HEPS_HUMAN	PRTC_CANFA	PRTC_CAPHI	PRTC_FELCA	PRTC_HORSE	PRTC_MACMU	KLKF_HUMAN	KLKD_HUMAN	PRTC_BOVIN	PRTC_PIG	PRTC_HUMAN	VSP1_BOTJA	VSP1_VIPLE	FA9_RABIT	FA9_RAT	FA9_MOUSE	COGS_HYPLI	TRY3_LUCCU	CTR2_VESCR	TRYP_SACER	TRYD_HUMAN	TRY5_AEDAE	KLK6_HUMAN	KLKC_HUMAN	TRYP_FUSOX	KLK9_HUMAN	KLKB_HUMAN	KLKE_HUMAN
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MISCELLANBOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.

-i - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. -i - SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

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CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
BLOOd Coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Live:
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use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See For send an email to license@isb-sib.ch).
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1; GLU_CARBOXYLATION; 1.
1; KRINGLE_1; 2.
5; KRINGLE_2; 2.
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InterPro; IPR000294; V1tK_dep_GLA.
Pfam; PF00061; Kringle; 2.
Pfam; PF00069; trypsin; 1.
Pfam; PF00094; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                            InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
                                                                                             IPR000001; Kringle.
IPR003966; Prothrombin.
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PRINTS; PR0018; RRINGLE.
PRINTS; PR01505; PROTHROMBIN.
PRODOM; PR000395; KRING1e; 2.
SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
SMART; SM00130; RR; 2.
                                       EMBL; X52835; CAA37017.1; -.
                                               EMBL; M81397; AAA42240.1; -. PIR; S10511; S10511.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-91025551; PubMed-2222810;
Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
Fitzgibbon J.J., Pai GNR, coding for mouse prothrombin and
localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
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                                                                                                                                                                                                                                                                                    Length 617;
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                                           SIMILARITY).
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-i- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
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101-NOV-1990 (Rel. 16, Last sequence update)
101-NOV-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
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larity 100.0%; Pred. No. 0.0
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                                                                                                                                                                                                                                             DR PROSITE; PS00011; GIU_CARBOXILATION; 1.

DR PROSITE; PS00011; GIU_CARBOXILATION; 1.

DR PROSITE; PS00021; KRINGLE_1; 2.

DR PROSITE; PS00040; TRYPSIN_DM; 1.

DR PROSITE; PS00134; TRYPSIN_DM; 1.

DR PROSITE; PS00135; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_HIS; 1.

W Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; W Hydrolase; Serine protease; Kringle; Signal.

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CLEAVAGE (BY FACTOR XA).
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GiA_blood.
InterPro; IPR0000001; Kringle.
InterPro; IPR0013966; Prothrombin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GiA.
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PRINTS; PR01505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
SMART; SM00020; Tryp_SPC; 1.
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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                       EMBL; X52308; CAA36548.1; -. EMBL; M81394; AAA40435.1; -. PIR; A35827; A35827. HSSP; P00734; LB7X.
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Pfam; PF00089; trypsin; 1.
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SEQUENCE OF 8-622 FROM N.A.
MEDLINE-83231469; PubMed-6305407;
Degen S.J.F., McGillivray R.T.A., Davie E.W.;
"Characterization of the complementary deoxyribonucleic acid and gene
                                                                                                                                                              Gaps
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MEDLINE-90059942, pubmed-2583108,
Bode W., Mayr I., Baumann J.,
The refined 1.9 A crystal structure of human alpha-thrombin:
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Prothrombin fragment 1 X 2 X 3, a major product of prothrombin activation in human plasma.";
J. Biol. Chem. 261:13210-13215(1986).
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Butkowski R.J., Ellon J., Dowahlog M.R., Mann K.G.;
"Primary structure of human prethrombin 2 and alpha-thrombin.";
J. Biol. Chem. 252:4942-4957(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECTION N.A., AND VARIANT MET-165.
Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L. O'zuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-77193964; PubMed-266717; Walz D.A., Hewett-Emmett D., Seegers W.H.; Hewett-Emmett D., Seegers W.H.; Admino acid sequence of human prothrombin fragments 1 and 2."; Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
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1-JUL-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II)
                                                                                                                               Length 618;
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                                                                                                                   Score 59; DB 1; Length or. Pred. No. 0.0062;
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B89F719AAFD601E0 CRC64;
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MEDLINE-87008532; PubMed-3759958;
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Biochemistry 22:2087-2097(1983)
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Best Local Similarity 100.

Matches 10; Conservative
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Cera E.;
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and thrombomodulin.";
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van de Locht A., Bode W., Huber R., le Bonniec B.F., Stone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for arginine at residue 273.";
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MEDLINE-93043342; Pubmed=1421398;
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Blood 80:2275-2280(1992).
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                                                                                                                                                                                                                                                                                             thrombin."
REPRESENTE EN PRESENTA DE LA PRESENT
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Henriksen R.A., Mann K.G.;

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BI. J. Haematol. 54:245-254(1993).

-I. THOMALIN. THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS FIBRINGEN TO FIRSHIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND. IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

-I. CATALYIC ACTIVITY: Preferential cleavage: Arg-1-Gly; activates fibrinogen to fibrin and releases fibrinopeptide A and B.

-I. SUBCELLULAR LOCATION: Extracellular.

-I. SUBCELLULAR LOCATION: Extracellular.

-I. PTW: THE GAMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS, RESULT FROM THE CARBOXYGLUTAMYL RESIDUES BY A MICROSOMAL ENTYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
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MATURAL BLOOD CLOTTING.

MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
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                                                                                                            MEDLINE-92378975; PubMed-1354985;
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Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
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fibrinogen bound to bovine thrombin at 2.3-A resolution.";
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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 -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO,
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Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
"Structure of bovine prothrombin fragment 1 refined at 2.25-A
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                        Length 622;
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MEDLINE-88245190; Pubmed-3379642;
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             Score 59; DB 1; Le
Pred. No. 0.0062;
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01-APR-1990 (Rel. 14, Last sequence update)
102-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                     625 AA.
                                               0; Mismatches
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Biochemistry 31:2554-2566(1992).
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                      100.0%;
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Best Local Similarity 100.
Matches 10; Conservative
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Trwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;

Irwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;

In Characterization of the Arrivares RACTORS V. VII, VIII, XIII,

IRRINGEN NO FIBRIN AND ACTIVARES RACTORS V. VII, VIII, XIII,

AND, IN COMPLEX WITH THROMBOMODULIN, PROFEIN C.

I. CATALYTIC ACTIVITY: Preferential cleavage: Argi-Gly; activates fibrinopen to fibrin and releases fibrinopeptide A and B.

I. SUBCELLULAR LOCATION: Extracellular.

I. SUBCELLULAR LOCATION: Extracellular.

I. SUBCELFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.

I. SUBCELFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.

I. PTM: THE GAMMA-CARBOXYLOTAMYL RESIDUES, WHICH BIND CALCIUM IONS,

RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES

CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN. MEDLINE-97102783; PubMed-8947023; van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C., Hoffken W., Huber R.;
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-92389319; PubMed-1518046;
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"Refined 2.3 A X-ray crystal structure of bovine thrombin complexes formed with the benzamidine and arginine-based thrombin inhibitors NARAP, 4-TARAP and MOPA. A starting point for improving antithrombotics.";
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Structure of the thrombin complex with triabin, a lipocalin-like
"Structure of the inhibitor derived from a triatomine bug.";
Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
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MEDLINE-98004486; PubMed-9342325;
Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
-1- DATABABAE: NAME—PROSYME technical fact sheet;
WWW-http://www.prozyme.com/technical/thrombindata.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The ornithodorin-thrombin crystal structure, a key to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 15:6011-6017(1996).
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PIR; S02537; S02537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease; Transmembrane; Signal-anchor.

1 161 NON-CATALYTIC CHAIN (POTENTIAL).
162 416 CATALYTIC CHAIN (POTENTIAL).
1 16 CYTOPLASMIC (POTENTIAL).
17 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           protease, hepsin, from mouse preimplantation embryos.";
J. Biol. Chem. 272:31315-31320(1997).
-!- FUNCTION: PLAYS AN ESSENTIAL ROLE IN CELL GROWTH AND MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LIRKED (GLCNAC. . .) (POTENTIAL).
N-LIRKED (GLCNAC. . .)
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
MEDLINE-98058912; PubMed-9395459;

Yu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.;

Yi T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.;

*Identification and cloning of the membrane-associated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease hepsin (EC 3.4.21.-).
                                                                                                   416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; SOL. 224; -:
MGD; MGI:1196620; Hpn.
InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001214; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00089; trypsin; 1.
PR001715; PR00722; CHYMOTRYPSIN.
SMART; SM00202; SR; 1.
FROSITE; PS50240; TRYPSIN_LDOM; 1.
PROSITE; PS00134; TRYPSIN_LSE; 1.
PROSITE; PS00134; TRYPSIN_LSE; 1.
Hydrolase; Serine protease; Transmembran.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF030065; AAB84221.1; -. HSSP; P00763; 1DPO.
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                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               OF CELL MORPHOLOGY
                                                                                                                                                                                                                  Mus musculus (Mouse)
 111111111
567 CEGDSGGPFV 576
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
                                                                                               HEPS_MOUSE
035453;
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DISULFID
CARBOHYD
SEQUENCE
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TRANSMEM
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                                                                                   HEPS_MOUSE
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                 유
                                                                                                   PROSITE: PSO0011; GLU_CARBOXXLATION; ...
PROSITE: PSO0011; KRINGLE_1; 2.
PROSITE: PSO0001; KRINGLE_2; 2.
PROSITE: PSSO240; TRYPSIN_DOM; 1.
PROSITE: PSO0134; TRYPSIN_LDM; 1.
PROSITE: PSO0135; TRYPSIN_SER; 1.
PROSITE: PSO0135; TRYPSIN_SER; 1.
BLOOG COAGULATION; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Ydrolase; Serine protease; Kringle; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 1; Length 625; 100.0%; Pred. No. 0.0063; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE (FRAGMENT ACTIVATION PEPTIDE (FRAGMENT THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
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GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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CLEAVAGE (BY THOMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CLARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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GAMMA-CARBOXYGLUTAMIC
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KRINGLE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00020; Tryp_SPc; 1.

E. PS00011; GLU_CARBOXYLATION; 1.

E. PS00011; KRINGLE_1; 2.

E. PS50070; KRINGLE_2; 2.
                                                                                                                                                                                                                                                                                         Interpro; IPR000001; Kringle...
Interpro; IPR0013966; Prothrombin.
InterPro; IPR001254; Ser_prothease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF000051; Kringle; 2.
Pfam; PF000089; trypsin; 1.
                                                                                                                                                                                                                                                           IPR001314; Chymotrypsin. IPR002383; GLA_blood.
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00594; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR01505; PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD000395; Kringle; 2
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SMART; SM00130; KR; 2.
SMART; SM00020; TIYP_S
                                                                                                                                                                          21-APR-97.
06-MAY-98.
17-JUN-98.
16-FEB-99.
                                               31-JAN-94,
31-JAN-94,
                                                                                                                                                                                                                                                           IPR001314;
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                                                                                                                                               14-0CT-96
                                                                                31-MAY-94
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Best Local Simi
Matches 10;
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PDB;
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Conservative

Similarity

Gaps

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Score 56; DB 1; Length 416; Pred. No. 0.014; 1; Mismatches 0; Indels

94.98; illarity 90.08; Conservative

Similarity 9; Conserva

Query Match Best Local S Matches

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01.NOV-1988 (Rel. 0), Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
An novel trypsin.1lke serine protease (hepsin) with a putative
Transmembrane domain expressed by human liver and hepatoma cells.";
Blochemistry 27:1067-1074(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF CELL MORPHOLOGY.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: PRESENT IN MOST TISSUES, WITH THE HIGHEST
--- LEVEL IN LIYER.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choù S.H., Kurachi K.;
"Hepsin, a cell membrane-associated protease. Characterization,
tissue distribution, and gene localization.";
J. Blol. Chem. 266:16948-16933(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isuji A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S.
                                                                                                                                                                                                                       417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE-91358502; PubMed-1885621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88209431; PubMed-2835076;
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EMBL; X07732; CAA30588.1; --
EMBL; X07002; CAA30058.1; --
PIR; S00845; S00845.
HSSP; P00763; IDPO.
MENOPS; S01.224; --
Genew; HGNC:5155; HPN.
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PRINES, PR00722, CHYMOTRYPSIN.
SMART; SM00202; SR; 1.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                       STANDARD;
                                                                                  348 CQGDSGGPFV 357
                               CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P05981;
                                                                                                                                                                                             HEPS_HUMAN
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MEDLINE-94318474; PubMed-8043441;

MURAKAWA M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;

MARAKAWA M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;

MURAKAWA M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;

region of mammalian protein C.";

Br. J. Haematol. 86:590-600(1994).

1. Haematol. 86:590-600(1994).

1. FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULARES BLOOD COAGULATION PROTEINS.

IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                                     protesse; Transmembrane; Signal-anchor.
162 NON-CATALYTIC CHAIN (POTENTIAL).
417 CATALYTIC CHAIN (POTENTIAL).
17 CYTOPLASMIC (POTENTIAL).
44 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1999 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
14-UN-2002 (Rel. 41, Last annotation update)
Vitamin K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                       SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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B2086FF661E551D7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 1; Length 417;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and VIIIa.
-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                        (POTENTIAL).
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Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
; TRYPSIN_DOM; 1.; TRYPSIN_HIS; 1.; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                 45011 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                     94.9%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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257
353
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349 CQGDSGGPFV 358
                                                                                                                                                                                                                                                                                                                                              112
417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CEGDSGGPFV 10
                                                             Hydrolase; Serine
                   PROSITE; PS00134;
PROSITE; PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.218;
                                                                                                163
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Q28278;
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ACT_SITE
ACT_SITE
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CARBOHYD
SEQUENCE
   PROSITE;
PROSITE;
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                                                                                              CHAIN
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PRIC_FELCA
                                     DISULFID
CARBOHYD
CARBOHYD
   ACT_SITE
DISULFID
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DISULFID
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SEQUENCE
                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                    028412;
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                                                                                            NON_TER
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   ELEEEES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
Vitamin R dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
                                                                                       CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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InterPro; IPRO01254; Ser_protease_Try.
InterPro; IPRO01254; Ser_protease_Try.
SMART; SMO0020; Trypsin, 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LBS; PARTIAL.
Blood_coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                       Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
NON_TER
                                                                                                                                                                                                                                                      Score 53; DB 1; Length 157;
Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
                                                                                                                                                                                                                      17262 MW; E8B1BACF49220DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 AA
PROSITE; PSS0240; TRYPSIN_DOM; 1.
PROSITE; PSO0134; TRYPSIN_HIS; PARTIAL.
PROSITE; PSO0135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                      89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D43752; BAA07809.1; -. HSSP; P04070; 1PCU.
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                            26
125
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capra hircus (Goat).
                                                                                                                                                               17
78
157
157 AA;
                                                                                                                                                                                                                                                                                                                                                                  121 CEGDSGGPMV 130
                                                                                                                                                                                                                                                                           Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                              1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRTC_CAPHI
Q28315;
                                                                                         ACT_SITE
ACT_SITE
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PRTC_CAPHI
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
 STTTTTTTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- CATALYTIC ACTIVITY: Degradation of blood coaqulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
Vitamin ** dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROC.
Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
Mammalia; Butheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID-9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PinterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SWART; SW00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood_coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                B89790F9954B610A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17142 MW; FBDC5BE2ECA74BB4 CRC64;
CHARGE RELAY SYSTEM
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                Score 53; DB 1;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 AA.
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                17251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D43750; BAA07807.1; -. HSSP; P04070; 1PCU.
                                                                                                                                                                                             89.8%;
90.0%;
                                                                                                                                                                    Query Match
Best Local Similarity 90...
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
78
157
157 AA;
                                                                                                                                                                                                                                                                                                                                         121 CEGDSGGPMV 130
                                                                                                                                                   157 AA;
                                                                                                                                                                                                                                                                                          1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.218;
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121 CEGDSGGPMV 130

Length 157;

5-DEC-1998 PRTC_HORSE Q28380;

PRTC_HORSE RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
M. A comparative study of partial primary structures of the catalytic region of mammalian protein C.;
Br. J. Haematol 86:590-600(1994)
- I. FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                                                                                                                                                       15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - - CATALYTIC ACTIVITY: Degradation of blood coagulation factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%; Score 53; DB 1; Length 161; 90.0%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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CHARGE RELAY SYSTEM.
BY STMILARITY.
N-LIRKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                            161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PSO0134; TRYPSIN HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001254; Ser_protease_Try. Pfam; PF00089; trypsin; 1. SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17770 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D43754; BAA07811.1; -. HSSP; P04070; 1PCU.
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                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AA;
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS: S01.218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and VIIIa
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KLKF_HUMAN
ID KLKF_HUMAN
                                                                                                                               PRTC_MACMU
Q28506;
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ACT_SITE
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGILATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BFAA6EA045C3C580 CRC64;
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                         DB 1;
0.018;
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SIMILARITY.
                                                                                Mismatches
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Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
                         Score 53;
Pred. No.
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90.0%;
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                         89.8%;
90.0%;
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Query Match
Best Local Similarity
'-hag 9; Conserv?
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9; Conserva
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Query Match Best Local S

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NON_TER SEQUENCE CARBOHYD

ACT_SITE DISULFID DISULFID

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SEQUENCE FROM N.A.
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KLK13 OR KLKL4.
                                                      VARSPLIC
CONFLICT
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                           PubMed-11010966;
Yousef G.M., Scorllas A., Jung K., Ashworth L.K., Diamandis E.P.;
Molecular clonding of the human kallikrein 15 gene (KIK15). Uprequilation in prostate cancer.";
J. Biol. Chem. 276:53-61(2001).
                                                                                                                                                                                                                         Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCualg J., Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                        SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE (POTENTIAL). KALLIKREIN 15.
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PROSITE: PS50240; TRYPSIN_DOW; 1.

PROSITE: PS00134; TRYPSIN_HIS; 1.

PROSITE: PS00134; TRYPSIN_HIS; 1.

PROSITE: PS00135; TRYPSIN_SER; FALSE_NEG.

Hydrolase: Serine protease; Glycoprotein; Signal; Zymogen; Alternative splicing.

SIGNAL 1 16 POTENTIAL.

PROPEP 17 21 ACTIVATION PEPTIDE (POTENTIAL CHAIN 22 256 KALLIKREIN 15.
         16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
Rallikrein 15 precursor (EC 3.4.21.-) (Aco protease).
Q9H2R6; Q9H2R4; Q9H2R3; Q9HBG9; Q15358;
                                                                                                                                                                                                                                                                                            PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20510030; PubMed-11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF243527; AAG33354.1; -.
BMBL; X75543; CAA53145.1; ALT_SEQ.
HSSP; P00763; 1DPO.
MEROPS; S01.081; -.
                                                                                                                                                                                                                                                                                                                   MEDLINE-94289486; PubMed-8018728;
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                                                                   Homo sapiens (Human)
                                                                                                  NCBI_TaxID-9606;
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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Robayashi A.,
Olsen A.S., Carrano A.V.;
Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIJNE-20229789; PubMed-10766816;
Yousef G.M., Chang A., Diamandis B.P.;
"Identification and characterization of KLK-L4, a new kallikrein-like gene that appears to be down-regulated in breast cancer tissues.";
J. Biol. Chem. 275:11891-11898(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKD HUMAN STANDARD; PRT; 2// AA. 097433; Cleated) CoCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41). Last amoration update) Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-11ke protein 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND
                                                                                                                                                                             SHNEPGTAGSPRSQ -> PLSSP (IN REF. 2)
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                   Score 53; DB 1; Length 256;
Pred. No. 0.029;
0; Mismatches 1; Indels
                                                                                                                                                                                                             B5EBF8D6022786B5 CRC64;
                                                            MISSING (IN ISOFORM 4)
MISSING (IN ISOFORM 2)
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MISSING (IN ISOFORM 3)
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EMBL; AC011473; AAC32559.1; -.
EMBL; AL050220; CAB43320.1; ALT_INIT.
HSSP; P00763; 1DPO.
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   171
232
206
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256 AA;
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Best Local Similarity
Matches 9; Conserv
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PROSITE; PS00134;
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                                                                                                                                                                                                                                                                                                                                                                                    and VIIIa.
                                                                                                                                                                                          PROCESSING,
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MEDLINE-85014826; Pubmed-6091100;
Long G.L., Balagaje R.M., McGillivray R.T.A.;
"Cloning and sequencing of 11ver cDNA coding for bovine protein C.";
Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
VNYPKTLQCAN -> GMHPHRWPEAP (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
13-ADG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyidae; Bovinae; Bos.
                                                                                                                                                                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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MEDLINE-83007325; PubMed-6896876;
Fernlund P., Stenflo J.
Farnlund F.

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Draktenberg T., Fernlund P., Roepstorff P., Stenflo J.;
Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53; DB 1; Length 277; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                    BA8A9E8DCFB5D542 CRC64;
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(BY
                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                              SMAKK; SMOUSES, TRIFESTN DOM; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
STRNAL 1 16
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BY SIMILARITY.
BY SIMILARITY.
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                                                Interpro: IRR001314; Chymotrypsin.
InterPro: IRR001254; Ser_protease_Iry.
Pfam; PF00009; trypaln; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
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MEDLINE-83007326; PubMed-6896877;
                                                                                                                                                                                                                                                                                                                                                                                                                                      30570 MW;
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90.0%;
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                HGNC: 6361; KLK13.
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214 CEGDSGGPLV 223
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                                     605505;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: SYMTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.
-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-1- THESUE SPECIFICITY PROMOTED BY THE MODIFIED PROTEIN TO BIND CALCIUM.
-1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN, THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;

"Structural changes required for activation of protein C are induced by Ca2+ binding to a high affinity site that does not contain gammacarboxyglutamic acid.";

J. Biol. Chem. 258:5534-5560(1983).

-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILLA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                        MEDINE-83213513: PubMed-6304092;
Esmon N.L., Debault L.E., Esmon C.T.;
"Proteolytic formation and properties of gamma-carboxyglutamic acid-
Stenflo J., Fernlund P.; "Amino acid sequence of the heavy chain of bovine protein C."; J. Biol. Chem. 257:12180-12190(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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EGF_2; 2.
EGF_CA1.
GLCARDAXIATION; 1.
TRYPSIN_DOM; 1.
TRYPSIN_HIS; FALSE_NEG.
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                                                                                                                                                       PROCESSING, AND CALCIUM-BINDING DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AND CALCIUM-BINDING DATA
                                                                                                                                                                                                                                                                                                               domainless protein C.";
J. Biol. Chem. 258:5548-5553(1983).
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EGF-like.
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PROSITE; PS00010; ASX_HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-83213514; PubMed-6406503;
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c. --- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The airgyme is then activated by thrombin, which cleaves a tetradecapeptide from the anino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

--- ISSUE SPECIFICITY: Plasma; synthesized in the liver.

--- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

--- INTELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

--- SIMILARITY: CONTRINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
GGFALL 18 BX SIMILARITY.
PROPEP 19 41 BY SIMILARITY.
CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.
CHAIN 42 196 PROTEIN C. LIGHT CHAIN (BY
                                                                        domains.";
Cell. Mol. Life Sci. 58:148-159(2001).
-!-FUNCTION: Protein C is a vitamin K-dependent serine protease that
-regulates blood coagulation by inactivating factors Va and VIIIa
in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                            *Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE (BY SIMILARITY). CLEAVAGE (BY THROMBIN) (BY
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InterPro: IPR00152; Asx_hydroxyl.
InterPro: IPR001512; Asx_hydroxyl.
InterPro: IPR001814; Chymctrpsin.
InterPro: IPR001881; EGF-Ia.
InterPro: IPR001881; EGF-Ca.
InterPro: IPR001284; SGT_blood.
InterPro: IPR001284; VItK_dep_GIA.
InterPro: IPR001294; VItK_dep_GIA.
InterPro: IPR00089; GIA.
InterPro: IPR001891; GIA.
InterPro: IPR001891; GIA.
InterPro: IPR001891; GIA.
InterPro: IPR001891; GIA.
INTERPS: PR001891; GIABLOD.
SMART; SM00181; EGF; Z.
SMART; SM00001; GIABLOD.
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00118; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LSE; 1.
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PS00010; ASX_HYDROXYL; 1.
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MEDLINE-21121490; PubMed-11229814;
Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
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16-OCT-2010 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin R dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 0.052;
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CAAF6833F894C209 CRC64;
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PROTEIN C HEAVY CHAIN.
ACTIVATION PEPTIDE.
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Matches 9; Conservative
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SIMILARITY). GGF-LIKE 1. GGF-LIKE 2.	SERINE PROTEASE. SAMMA-CARBOXYGLUTAMIC ACID (BY STATT STOTTON	STHILARITY) STANMA-CARBOXYGLUTAMIC ACID (BY STHILARITY) SANMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY). SAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).	ACID	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY). HYDROXYLATION (BY SIMILARITY). CHARGE RELAY SYSTEM. CHARGE RELAY SYSTEM. EHRGE RELAY SYSTEM. BY SIMILARITY.	BY SIMILARITY. N'LINKED (GICNAC) (POTENTIAL). N'LINKED (GICNAC) (POTENTIAL). B541AAC14C16D09 CRC64; SCOPE 53: DB 1: Length 459:	red. No. 0.052; Mismatches 1; Inde
	DOMAIN 214 459 MOD_RES 47 47	MOD_RES 48 48 MOD_RES 55 55	MOD_RES 57 57 MOD_RES 60 60 MOD_RES 61 61	MOD_RES 66 66 MOD_RES 67 67	MOD_RES 70 70 MOD_RES 112 112 ACT_SITE 255 255 ACT_SITE 400 400 DISULRID 58 63	DISULFID 91 110 DISULFID 100 105 DISULFID 104 119 DISULFID 124 119 DISULFID 139 150 DISULFID 146 159 DISULFID 161 174 DISULFID 161 174 DISULFID 240 256 DISULFID 371 385 DISULFID 371 385 CARBOHYD 292 292 CARBOHYD 292 292 CARBOHYD 353 353 SEQUENCE 459 AA; 51866 MW;	Similarity 90.0%; 9; Conservative 0

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Human prostate spe Antigen peptide de Antigen peptide de Drosophila melanoy Mature kallikrein Prostate-specific Human prostate spe Prostate-specific	numan prostate spe
QΙ	AAW58061 AAW58062 AAW11019 ABB66284 AAR77098 AAR77098 AAW53213 AAW53213	AAW9618/
图	110 110 110 110 110	70
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Monoclonal antibodies specific for prostate specific antigen - useful, e.g. in screening for prostate or breast cancer and especially to distinguish between benign prostatic hyperplasia and

WPI; 1998-193789/17.

Heavner GA;

	11	47 9	4.0	237	21	AAB11041		Human prostate-spe
	12			237	22	AAB19818		Prostate specific
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	4.	~ r		240	9 6	AAWLIU23		prostate
	15			0 4 0	3 5	APR 5005		phila mela
	17			250	12	AAW03130		Prostate-specific
	18	. ~	94.0	252	55	ABB63479	,	Drosophila melanog
<u>.</u>	19	٠		255	77	AAB21313		
	20	r 1		257	22	AA006276		Prostate specific
	21	- r		200	7 (ABBORGIR		Drosophila melanog
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	2 4			412	22	ABB62250		
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i X	200	1			,			
O	Human	prostate		specific	anti	antigen peptide	le SEQ ID NO:79.	
Ž	Human	prostate		specific		antiqen; PSA;	epitope; monoclonal	lonal antibody;
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S. O.	Synthetic	tic.						
so	HOMO S	saptens						
PN	WO9810292	292-A1						
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PF	25-AUG	-AUG-1997;	974	97WO-US14909	606			
PR	06-SEP	-SEP-1996;	39E	96US-0025404	404			
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A X			, ,	2	•			

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rue productional antibodies specific for PSA and hybridomas producing them have been developed. The antibodies: (a) bind to free PSA; (b) are monoclonal antibodies: (a) bind to free PSA; (b) are monoclonal antibodies 10, 11, 16 or 22.2 and cragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and cor fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and 15.2, 156 or 225 binding to amino acids 139-144 (EELFITP) and 55-60 (SLFHPE) respectively of free and bound PSA, or fragments. The antibodies are useful to detect PSA. For detecting free PSA only, an immunoassay comprising a solid support with attached labelled monoclonal antibody specific for free PSA (especially (b)) and a PSA standard can be used: To detect both free and bound PSA, a second solid support with attached (differently labelled) monoclonal antibody binding free and bound PSA (especially selected from (c)) can be used either with, or in place of, the first solid support. The antibodies are useful in cancer screening, especially prostate and breast cancer. By obtaining total and free PSA (values, their ratio can be used to separate prostatic cancer. (Pca) from Collagin prostatic hyperplasia (BHP) patients. Measurement of PSA is also antibodies allow evaluation of PSA free/total ratio, enabling separation cof BPH and PCA patients with PSA values 4-10 ng/ml not previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate specific antigen; PSA; epitope; monoclonal antibody; detection; cancer; serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibodies specific for prostate specific antigen useful, e.g. in screening for prostate or breast cancer and especially to distinguish between benign prostatic hyperplasia and
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW58062 standard; peptide; 15 AA.
                                   Example; Page 63; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.0%;
80.0%;
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AA;
   prostate cancer
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9810292-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Example; Page 63; 84pp; English

prostate cancer

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The present sequence represents a prostate specific antigen (PSA)

peptide. Monoclonal antibodies specific for PSA and hybridomas producing them have been developed. The antibodies: (a) bind to free PSA; (b) are monoclonal antibody 365 binding to amino acids 82-87 of free PSA; (b) are monoclonal antibodies 10, 11, 16 or 22.2 and 15.2, 156 or 22.5 binding to amino acids 139-144 (EELETP) and 55-60

CSEPHPE) respectively of free and bound PSA, or fragments. The antibodies are useful to detect PSA. For detecting free PSA only, an immunoassay comprising a solid support with attached labelled monoclonal antibody specific for free PSA (especially (b)) and a PSA standard can be used. To detect both free and bound PSA, a second solid support with attached (differently labelled) monoclonal antibody binding free and bound PSA (especially selected from (c)) can be used either with, or in place of, the first solid support. The antibodies are useful in cancer screening, especially prostate and breast cancer. By obtaining total and free PSA values, their ratio can be used to separate prostatic cancer (PCa) from beingen prostatic hyperplasia (BHP) patients. Measurement of PSA is also useful after radical prostatectomy, to predict disease persistence. The antibodies allow evaluation of PSA free/foral ratio, enabling separation of BBH and PCA patients with PSA values 4-10 ng/ml not previously
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a novel peptide which has 20 contiguous amino acids derived from the 240 residue sequence of the human prostate specific antigen (PSA) (see AAW11023). The preferred peptide has two hydrophobic regions and one hydrophilic region each of about 5 as in length, arranged as follows: hydrophobic-hydrophilic-hydrophobic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen peptide derived from prostate specific antigen - does not cross react with related kallikreins, for diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSA; kallikrein; prostate cancer; antigenic; polyclonal antisera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen peptide derived from human prostate specific antigen.
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Pred. No. 10;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW11019 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Matches 8; Conservative
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us-09-909-348-2.rag

160 CSGDSGGPLV 169

AAR84671 standard; Protein; 237 AA.

serine protease; prostate-specific antigen;

prostate cancer; diagnosis.

Homo sapiens.

WO9530758-A1

16-NOV-1995

Kallikrein hK3;

Mature kallikrein hK3

04-MAR-1996

AAR84671;

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
Polyclonal antisera specific for the antigenic peptide may be used in method for diagnosing prostate cancer in vivo or in vitro. The peptide represents a sequence unique to PSA which does not cross react with certain kallikreins.
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                         Score 47; DB 18; Length 20;
Pred. No. 13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 25644.
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Best Local Similarity 80.0%;
Matches 8; Conservative
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ilarity 80.0%;
Conservative
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11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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N-PSDB; ABL10387.
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Matches 8; Conserv
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ABB66284
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Young CYF;

WPI; 1995-404123/51.

95US-0427767.94US-0241174. 95WO-US06157

02-MAY-1995; 10-MAY-1994;

09-MAY-1995;

(HYBR-) HYBRITECH INC. (MAYO-) MAYO FOUNDATION. Saedi MS, Tindall DJ,

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Gaps
    S
                                                                                                                Human kallikrein hK3 (AAR84671) is a prostate-specific kallikrein showing homology to prostate-specific glandular kallikrein hK2 (AAR84667). Nonhomologous regions of the kallikreins can be used for prepn. of antibodies specific to hK2.
New isolated prostate-specific kallikrein polypeptide(s) - used to develop prods. for use in assays for such polypeptide(s), partic. for diagnosis and monitoring of prostate cancer
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                                                                                                                                                                                                                                                                  94.0%; Score 47; DB 16; Length 237; 80.0%; Pred. No. 84; 2; Indels ive 0; Mismatches 2; Indels
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                                                                                    Disclosure; Page 31; 61pp; English:
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185 CSGDSGGPLV 194
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Gaps

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1 CXGDSGGPXV 10

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oligonucleotides to amplify the DNA by PCR to yield amplified hK2 DNA, where the conditions amplify the DNA obtained by RT of RNA from at lea
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                                                                                                      237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a diagnostic method for detecting human kallikrein 2 (hK2) DNA. The method comprises: (a) contacting DNA obtained by reverse transcription (RT) of RNA from a human physiological sample which comprises cells suspected of containing hK2 RNA with at least 2
                                                                                                                                                                                                                    A prostate-specific antigen (PSA) is detected by isolating mRNA from a sample, producing cDNA, and subjecting the cDNA to RT-PCR using primers specific for the human PSA coding region (given in AAT04864).
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                      Method for enhancing prostate-specific antigen detection - provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate cancer; detection; hK2; hK1; hK3; phK2; tissue kallikrein; pphK2; prostate-specific glandular kallikrein protein; PSA; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of human kallikrein 2 RNA - by reverse transcription amplification by PCR, for detecting, monitoring and staging of
                                                                                                                                                                    sensitive means to identify early stages of prostate cancer
                                                                                                                                                                                                                                                                                                   16; Length 237;
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                                                                                                                                                                                                                                                                                               DB 7
84;
                                                                                                                                                                                                                                                                                                   Score 47; DB 1
Pred. No. 84;
0; Mismatches
                                                                                          Raffo A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate-specific antigen protein hK3.
                                                                                                                                                                                           Disclosure; Page 69-70; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young CYF;
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                                                                                          Olsson CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW83213 standard; Protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                               (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                   94.0%;
80.0%;
            95WO-DS04680
                                      94US-0229391
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                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US07027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate-specific antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tindall DJ,
                                                                                                              WPI; 1995-373812/48.
N-PSDB; AAT04864.
                                                                                         Katz AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-594592/50.
                                                                                                                                                                                                                                                                                                                                                                               185 CSGDSGGPLV 194
                                                                                                                                                                                                                                                                                                                                                       CXGDSGGPXV 10
                                                                                                                                                                                                                                                                         237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer
                                      15-APR-1994;
            14-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Slawin KM,
                                                                                       Buttyan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW83213;
                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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Monoclonal antibodies specific for PSA and hybridomas producing them have been developed. The antibodies: (a) bind to free PSA; (b) are monoclonal antibody 365 binding to amino acids 82.87 of free PSA (IRNRFL) component antibody 365 binding to amino acids 81.87 of free PSA (IRNRFL) or fragment, and (c) are monoclonal antibodies 10, 11 16 or 22.2 and 15.2, 156 or 225 binding to amino acids 139-144 (EELFITP) and 55-60 (SIEMPE) respectively of free and bound PSA, or fragments. The antibodies are useful to detect PSA. For detecting free PSA only, an immunosasay comprising a solid support with attached labelled monoclonal antibody specific for free PSA (especially (b)) and a PSA standard can be used. To detect both free and bound PSA, a second solid support with attached (differently labelled) monoclonal antibody binding free and bound PSA (especially prostate and bound PSA) as escond solid support. The antibodies are useful in cancer screening, especially prostate and breast cancer. By obtaining total and free PSA (especially prostate and breast cancer. By obtaining total and free PSA (especially prostate and breast cancer. By obtaining total and free PSA (especially prostate and breast cancer. By obtaining total and free PSA (especially prostate and breast cancer. By obtaining total and pressistence. The benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also useful after radical prostatectomy, to predict disease persistence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
one cell containing hK2 in a sample which comprises at least 107 to 109 cells; and (b) detecting the presence of the amplified hK2 DNA. The method can be used for detecting, monitoring the progression of and pathologically staging prostate cancer. The present sequence represents prostate-specific antigen protein hK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific antigen; PSA; epitope; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful, e.g. in screening for prostate or breast cancer and especially to distinguish between benign prostatic hyperplasia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents prostate specific antigen (PSA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibodies specific for prostate specific antigen
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 19;
Pred. No. 84;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruman prostate specific antigen protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olsclosure; Page 32-33; 84pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW56086 standard; Protein; 237 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                        94.0%;
80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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80.08;

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Best Local Similarity 80.0
Matches 8; Conservative
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 antibodies allow evaluation of PSA free/total ratio, enabling separation of BPH and PCa patients with PSA values 4-10~\rm ng/ml not previously possible by total PSA testing, avoiding biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises human prostate-specific antigen (PSA)

Chr3. PSA levels are widely used as a prognostic indicator of prostate carcinoma. The invention provides a novel diagnostic method comprising contacting antibodies that specifically bind to method comprising contacting antibodies that specifically bind to human prostate-specific glandular kallikrein protein hRZ (see WA53950 or pro-hRZ (phKZ, see AAW45396), but not with PSA, with a sample of physiological fluid from a human. The assay is based on the discovery that phKZ is detected in the supernatant of a prostate carcinoma cell line and that hKZ is present in human physiological fluid from prostate cancer cells. The method is useful for monitoring the treatment and/or progression of prostate cancer in males that have believed the early detection of prostate cancer in males that chave BPH or a high grade prostatic neoplasia (HPGN) or whose family members have or had BPH, HPGN or a prostate cancer. Anonitoring the
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           presence and/or amount of hK2 complexes with plasma proteins may also be important in distinguishing between prostate cancer and BPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnostic methods using antibodies which bind prostate antigens useful for, e.g. monitoring treatment or progression of prostate % \left( 1\right) =1
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate-specific antigen; hK3; PSA; human; hK2; prostate-specific glandular kallikrein; prostate carcinoma; prostate cancer; benign prostatic hyperplasia; diagnosis.
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                                                                                                   DB 19; Length 237;
84;
                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Prostate-specific antigen protein hK3 (PSA).
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 55-56; 100pp; English.
                                                                                                          Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grauer L, Klee GG, Mikolajczyk SD,
                                                                                                                                                                                                                                                                                                       AAW45398 standard; Protein; 237 AA.
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                                                                                                          94.0%;
80.0%;
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                                                                                         Ouery Match
Best Local Similarity 80...
Best Good 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-120378/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human kallikrein 2 (hK2) is expressed at elevated levels relative to
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of human kallikrein 2 - as a marker for developing products for
the diagnosis, prognosis, monitoring and treatment of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection;
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84;
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                            Indels
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treatment; monitoring; prostate specific antigen; PSA
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Pred. No. 84;
0; Mismatches
ed. No. 84;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 33-34; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate specific antigen (PSA).
                                                                                                                                                                                                                                                       AAW96187 standard; Protein; 237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young CYF;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monitoring hK2 levels
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Best Local Similarity
'Thea 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-105632/09.
N-PSDB; AAX08947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TIND/) TINDALL D J. (YOUN/) YOUNG C Y F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 CSGDSGGPLV 194
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                                                                              1 CXGDSGGPXV 10
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RESULT 11

DB 19; Length 237;

94.0%; Score 47;

Query Match

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Novel prostate specific antigen (PSA) for distinguishing benign prostatic hyperplasia from prostate cancer, comprises a clip at lysine 182 of the amino acid sequence of a mature form of PSA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a mature form of a novel form of prostate specific antigen (PSA). This form of PSA has at least 1 clip at Lys-182 and may additionally have 1 or more clips at Lys-1, Lys-145 and Lys-146. Preferably, the PSA contains at least 2 clips at Lys-145 and Lys-182. The novel forms of PSA exist at an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate specific antigen; PSA; BPSA; benign prostatic hyperplasia; BPH; marker; diagnosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prostate specific antigen specific to benign prostatic hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elevated level in patients suspected of having benign prostatic hyperplasmia (BPH) and therefore may be used as a serum marker or an immunohistological marker to help distinguish BPH from prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer. Antibodies recognising the novel forms of PSA and immunoassays that detect and determine the novel forms of PSA are
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    /note= "site of internal peptide bond cleavage"
                                                /note= "site of internal peptide bond cleavage"
                                                                                             peptide bond cleavage'
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182
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                                                                                                                                                                                                                                                                                                                                                                                                          Slawin K;
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                                                                                                                                                                                                                                                                                                                                                                                                          Wolfert R,
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Pred. No. 84;
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                                                                                             "site of internal
                                                                                                                                                                                                                                                                                                                                                                                                       Wang I, Rittenhouse H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB19819 standard; Protein; 237 AA.
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                                                                                                                                                                                                                                                                                                                                (HYBR-) HYBRITECH INC. (BAYU) BAYLOR COLLEGE MEDICINE
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80.0%;
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Best Local Similarity
These 8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Mikolajczyk S,
                                                                                                                                           WO200066718-A1
                          Cleavage-site
                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also provided
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                                                                                                                                                                                                                                                                                    30-APR-1999;
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                                                                                                                                                                                          09-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB19819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel composition (A) having a total socientation of prostate-specific antigen (PSA). (A) is useful as a reference in methods for detecting PSA (a marker for prostatic cancer) in human blood or serum and to generate isoform-specific monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies (MAb) against PSA, for use in immunological assays. (A) contains all the isoforms of PSA and can be isolated without significant formation of artefacts by autoproteolysis. Antibodies specific for particular PSA isoforms can improve diagnostic specificativ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition containing isoforms of prostate-specific antigen, useful a reference standard for analysis and for producing isoform-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                           Prostate-specific antigen; PSA; human; detection; prostatic cancer; isoform-specific monoclonal antibodies; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate specific antigen elevated in benign prostatic hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     benign prostatic hyperplasia; BPH; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 21; Length 237;
Pred. No. 84;
); Mismatches 2; Indels
                                                                                                                                                                 Human prostate-specific antigen N-terminal fragment #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SERA-) SERATEC GES BIOTECHNOLOGIE MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB19818 standard; Protein; 237 AA.
                      AAB11041 standard; peptide; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate specific antigen; PSA; marker; immunoassay; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.0%;
80.0%;
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                                                                                                                   (first entry)
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Volk M, Mast W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Cleavage-site
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                                                                                                                   08-FEB-2001
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                                                                    AAB11041;
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AAB19818
AAB11041
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Gaps

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WPI; 2002-527524/56.
N-PSDB; ABK86205.
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                                                                                                                                                          240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200240059-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2002
                                                                                                                                                                                                                                                                                                                                 AAU98921;
                                                                                                                                                            Sequence
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                                  8 x 5 5 5 5 5 5 5 5 5 5 5 8 8
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                                                                                                                                                                                          Distinguishing prostate cancer from benign prostatic hyperplasia using different forms of prostate specific antigen contained in a sample involves mathematically combining amounts of ProPSA and BPSA -
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                           The present sequence represents a mature form of a novel form of prostate specific antigen (PSA). This form of PSA has at least 1 clip at Lys-182 and may additionally have 1 or more clips at Lys-14. EPSA, a form of PSA that comprises at least clip at Lys-182, exists at an elevated level in the transition zone of benign prostatic hyperplasmia (BPH) tissue, compared to peripheral zone cancer and non-cancer prostate tissues. A method for distinguishing prostate cancer from BPH involves determining the ratio of proPSA and BPSA in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen peptide derived from prostate specific antigen - does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSA; kallikrein; prostate cancer; antigenic; polyclonal antisera
/note= "site of internal peptide bond cleavage"
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                Slawin K;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 237
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                Wolfert R,
                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB Pred. No. 84; 0; Mismatches
                                                                                                                                                Rittenhouse H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kokolus WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW11023 standard; Protein; 240 AA.
                                                                                                                                                                                                                                        Disclosure; Fig 14; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate specific antigen
                                                                                                                                                                                                                                                                                                                                                                                                   94.0%;
80.0%;
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                                                                   12-APR-2000; 2000WO-US09789
                                                                                          99US-030333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                Wang T,
                                                                                                               (HYBR-) HYBRITECH INC. (BAYU ) BAYLOR COLLEGE
                                                                                                                                                                      WPI; 2001-007264/01.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                               237 AA;
                                                                                                                                                Mikolajczyk S,
                      WO200067030-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fritsche HA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1996;
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                                                                                          30-APR-1999;
                                             09-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Human; prostate specific antigen; PSA; cytostatic; antiviral; immunostimulant; cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancreatic cancer; lymphoma; leukaemia; hepaduavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus.
                                                                                                                                                                            which is used to produce novel peptides derived from the 240 residue sequence. The preferred peptides have two hydrophoble regions and one hydrophilic regions each of about 5 as in length, arranged as follows: hydrophobic-hydrophilic-hydrophobic. Polyclonal antisera specific for the antigenic peptides may be used in a method for diagnosing prostate cancer in vivo or in vitro. The peptides represent a sequence unique to PSA which does not cross react with certain kallikreins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps.
                                                                                                                                                   The present sequence represents human prostate specific antigen (PSA)
react with related kallikreins, for diagnosis of prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
61.750
/note- "This region is specifically claimed"
/note- "This region is specifically claimed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 18;
Pred. No. 84;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMBI-) AMERICAN FOUND BIOLOGICAL RES INC. MINC, MINCHEFF M S.
LOUK/) LOURINOV D I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zoubak S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU98921 standard; Protein; 245 AA.
                                                                                       Claim 1; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001; 2001WO-US45626
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.00,
Dest Local Similarity 80.00,
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Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen by a cell, comprises administering a polynucleotide encoding a variant of an antigen

Claim 15; Page 122-123; 146pp; English.

response against a cell comprising a target antigen (1) in a subject, treatting a subject having undesired cells, for example tumour cells or virally infected calls (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynuclectide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and infections such as those caused by hepadnaviruses, lentiviruses (Including human immunodeficiency virus (HIV)), herpesviruses and the flaviviruses and pestiviruses. The present sequence represents the human prostate specific antigen (PSA) variant which has the signal sequence deleted, used as a target antigen in the method of the The invention relates to a method of inducing a cell-mediated immune

245 AA; Sequence

ö Query Match
Best Local Similarity 80.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 2; Indels

1 CXGDSGGPXV 10

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Search completed: May 12, 2003, 15:36:03 Job time: 29.6 secs

App11 App11

OM protein

Run on:

Sequence:

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Sequence 2, Appli
Sequence 2, Appli
Patent No. 5352664
                                                                                Sequence 2, A Sequence 77, Sequence 77,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Kokolus, William J.
APPLICANT: Fritsche, Herbert A.
APPLICANT: Fritsche, Herbert A.
APPLICANT: Tritsche, Dennis A.
TITLE OF INVENTION: IMMUNGENIC PEPTIDES OF PROSTATE
TITLE OF INVENTION: SPECIFIC ANTIGEN
NUMBER OF SEQUENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,228A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATONNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
RESERROCE/DOCKET NUMBER: J7,642
RELERROCE/DOCKET NUMBER: UTSC:388
TELERROCHIONICATION INFORMATION:
TELERAK: (512) 418-3000
TELERAK: (512) 474-7577
                                                                                US-08-981.088-2
US-08-330-594-8
US-08-482-130C-77
US-08-482-130C-77
US-08-906-77
US-08-906-616-77
US-08-906-616-77
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Pred. No. 0.12;
0; Mismatches
                     US-08-596-405-2
US-08-877-620-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America 2IP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08472228A
Patent No. 5807978
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Best Local Similarity 80.0%;
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
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Houston
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US-08-472-228A-19
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                                                                                                                                                                                       (without alignments)
30.649 Million cell updates/sec
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Sequence 19,
Sequence 11,
Sequence 2,
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                                                                                                                                                                 May 12, 2003, 15:33:37 ; Search time 9.6 Seconds
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
                        GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-472-228A-19
US-09-146-831-19
US-08-096-09303-19
US-08-08-096-946-11
US-08-08-768-8547-2
US-08-768-8547-2
US-08-768-8547-1
US-08-768-8547-1
US-08-944-483-38
US-09-104-248-38
US-09-303-339-2
US-09-303-339-2
US-09-303-339-2
US-09-303-339-2
US-09-303-319-2
US-09-303-319-2
US-09-44-831-1
US-08-472-228A-1
US-08-944-483-47
US-08-944-483-47
US-09-0102-732-5
US-09-0102-732-5
US-09-012-732-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match
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Pred. No. 1.1;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies Specific for Human
Prostate Glandular Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Amino acid sequence of PSA (hK3)
US-08-096-946-11
                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 1016.62-US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: Merchant & Gould
3100 No. 5516639west Center
    APPLICATION NUMBER: PCT/US96/09303
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,228
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/096,946
FILING DATE: 19930722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 5540z

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

ANDIUM TYPE: TBM PC COMPATIBLE

ANDITYPER: TBM PC COMPATIBLE
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                              FILING DATE: 07-JUN-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           20 amino acids
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                ; TOPOLOGY: linear
PCT-US96-09303-19
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                                          CLASSIFICATION:
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                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                              IMMUNOGENIC PEPTIDES OF PROSTATE SPECIFIC ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
UNRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.0%; Score 47; DB
80.0%; Pred. No. 0.12
tive 0; Mismatches
                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,228
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application PC/TUS9609303
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            Sequence 19, Application.US/09146831
Patent No. 6326471
                                                                                                                                                                       APPLICANT: Fritsche, Herbert A APPLICANT: Johnston, Dennis A. TITLE OF INVENTION: IMMUNGENIC TITLE OF INVENTION: SPECIFIC AN NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-1995
NTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-146-831-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CSGDSGGPLV 13
4 CSGDSGGPLV 13
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                                                                                                                                                                                                                                                                                                                                                   Texas
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
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Sequence 1, Application US/08768859A
Patent No. 6013471
GENERAL INFORMATION:
APPLICANT: Toung, Charles Y.F.
APPLICANT: Saedi, Mohammed S.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 21
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lundberg, Woessner & Kluth, P.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55402

MODPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,547
FILING DATE:
                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
RESISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43677-Á-PCI/JPW/MJG
FELECHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/768,859A
FILING DATE: 17-DECEMBER-1995
                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 237 amino acids TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid
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NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,4
REFERENCE/DOCKET NUMBER:
                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman,
STREET: P.O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 612-339-3061
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-718-547-2
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 185 CSGDSGGPLV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Minr
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-768-859A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TITLE OF INVENTION: A Method For Molecular Staging Of TITLE OF INVENTION: Prostate Cancer NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 237;
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: RAIZ, ABIOD E., et al.
TITLE OF INVENTION: A Method For Molecular Staging Of
TITLE OF INVENTION: Prostate Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/844,024
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,391
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wilte, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4367:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEKX: (212) 664-0525
TELEKX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                            Sequence 2, Application US/08844024
Patent No. 5840494
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-844-024-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
      185 CSGDSGGPLV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                           US-08-844-024-2
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NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 237;
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                       Lundberg, Woessner & Kluth, P.A.
                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,046B
FILLING DATE: 26-MARCH-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.1, 0; Mismatches
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTAATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 476.001US1
FELECOMMUNICATION INFORMATION:
                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLPITTS, TRACEY L. FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDWARD N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRANADOS, EDWAR
KLASS, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      : 612-373-6903
612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Est Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                       ADDRESSEE: Schwegman, STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott La
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MEDIUM TYPE: Diskett
                                                           Minneapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |||||| |
185 CSGDSGGPLV 194
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 60064-3500
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                                                                              STATE: 1
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                                                                                                                                                                                                                                                                            Sequence 1, Application US/08767820A
Patent No. 6093796
GENERAL INFORMATION:
APPLICANT: Tindall, Donald J.
APPLICANT: Seadl, Mohammed S.
ATITLE OF INVENTION: DAM Encoding HK2 Variant Polypeptides
NUMBER OF SEQUENCES: 21
                                                                          Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                            ALDINESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938 CITY: Minneapolis STATE: MN
                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Saedi, Mohammed S.
APPLICANT: Mikolajczyk, Stephen D.
TITLE OF INVENTION: Stable Variant HK2 Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,820A
FILING DATE: 17-DECEMBER-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFRENCE/DOCKET NUMBER: 545.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                          94.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-768-859A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 CSGDSGGPLV 194
                                                                                                                                                                             GENERAL INFORMATION:
                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                       1 CXGDSGGPXV 10
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                                                                                                                                                                                                                                                RESULT 8
US-08-767-820A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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                                                                                                                                                                                                                 DB 4; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application PC/TUS9407329
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical
APPLICANT: Education and Research
TITLE OF INVENTION: Antibodies Specific for Human
TITLE OF INVENTION: Prostate Glandular Kallikrein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUTRY: USA
ZIP: 55402
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 5;
Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Amino acid sequence of PSA (hK3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                       0; Mismatches
                    APPLICATION NUMBER: US/09/303,339
FILING DATE: 1999-04-30
                                                                                                                                                                                                                 94.0%; Score 47;
80.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3500 IDS Center
80 South Eighth Street
FILE REFERENCE: 451D-1875
CURRENT APPLICATION NUMBER: US/09/3
CURRENT FILING DATE: 199-04-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
ENGIH: 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RABSCH, Kevin W.
REGISTATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.0%;
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Best Local Similarity 80...
3; Conservative
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Best Local Similarity 80.0.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-09-303-339-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 CSGDSGGPLV 194
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                                                                                                                                                                                                                                                                                            1 CXGDSGGPXV 10
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STREET:
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Association with Prostate Tissues From Prostate Peripheral Zone
Zone
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; GENERAL INFORMATION:
    APPLICANT: Tindall, Donald J.
    APPLICANT: Klee, George G.
    TITLE OF INVENTION: Method for detection of breast cancer; TITLE OF INVENTION: Method for detection of breast cancer; TITLE OF INVENTION: MAGER: US/09/100,264
    CURRENT FILING DATE: 1998-06-19
    EARLIER APPLICATION NUMBER: US 60/050,963
; SALIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                              Length 237;
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Pred. No. 1.1;
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Pred. No.
                                                                                                                                      6183.US.01
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; Patent No. 6423503
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mikolajczyk, Stephen
APPLICANT: Wang, Tang
APPLICANT: Harry, Rittenhouse
APPLICANT: Robert, Wolfert
                                                                                               NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 616
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPAX: 847/938-2623
                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: No. 6232456e
US-08-944-483-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.0%;
80.0%;
                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 CSGDSGGPLV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 CSGDSGGPLV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXGDSGGPXV 10
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3
LENGIH: 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-303-339-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 240;
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB Pred. No. 1.1; 0; Mismatches
                                                  JUNEAR APPLICATION DATA:
APPLICATION NUMBER: US/08/472,228A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: May 12, 2003, 15:40:37 Job time: 11.6 secs
                                                                                             FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTATION UNDHER: 37,642
REFERENCE/DOCKET UNDHER: UTSC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 antho acids
TYPE: antho acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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MOLECULE TYPE: protein

US-08-472-228A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |||||| |
188 CSGDSGGPLV 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rokolus, William J.
APPLICANT: Fritsche, Herbert A.
APPLICANT: Fritsche, Dennis A.
APPLICANT: TINENCH, Dennis A.
TITLE OF INVENTION: IMMUNGENIC PEPTIDES OF PROSTATE
TITLE OF INVENTION: SPECIFIC ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06157
                                                                                                                                                                                                                                               E: Schwegman, Lundberg & Woessner, P.A 3500 IDS Center
                                                                         Mayo Foundation for Medical Education and Research
                                                                                                               APPLICANT: Hybritech Incorporated
APPLICANT: Tindall, Donald J.
APPLICANT: Young, Charles Y.F.
APPLICANT: Saedi, Mohammed S.
TITLE OF INVENTION: Recombinant HK2 Polypeptide
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ed. No. 1.1 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                Sequence 1, Application PC/TUS9506157
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08472228A
Patent No. 5807978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNET/AGENT INFORMATION:
NAME: REASCh, Revin W.
REGISTRATION NUMBER: 35,561
REFERENCE/DOCKET NUMBER: 150
TELECOMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35,561
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80.0%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-06157-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                       Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 CSGDSGGPLV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Texas
COUNTRY: Unit
                                                                                                                                                                                                                                                                                                                                                  55402
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                                                                                                                                                                                                                                                                                                            STATE: M
COUNTRY:
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                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                     STREET:
RESULT 14
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App11

Sequence 6, Sequence 247

Sequence

Sequence

Sequence 4, Appli Sequence 4, Appli Sequence 4, Appl

Scoring table:

Searched:

OM protein

Run on:

Minimum DB Maximum DB

Database

Result è

Sequence 16, Sequence 2, A Sequence 4, A Sequence 33, Sequence 18, Sequence 18,

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Sequence 2, Sequence 18, Sequence 19, Sequence 33, Sequence 34,
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 9; Length 261;
Pred. No. 1.3;
                                     US-10-050-611-2
US-10-125-459-18
US-10-125-459-19
US-10-067-761-34
US-10-067-761-34
US-09-904-090-2
US-09-904-090-2
US-09-904-090-2
US-09-904-156-33
US-09-946-633-18
US-09-946-633-19
                                                                                                                                                                                                                  US-10-050-692-4
US-10-050-688-4
US-09-909-122-4
US-09-885-441-6
                                                                                                                                                                                                                                                                            US-09-826-290-247
US-10-045-170A-16
US-10-044-708A-29
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 946, Application US/09895793 Publication No. US20020192763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
                                                                      Skeiky, Yasir A.W. Hepler, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-895-793-946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hural,
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LENGTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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Sequence 946, App
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Sequence 4, Appli
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                May 12, 2003, 15:38:52; Search time 19.4 Seconds (without alignments) 47.436 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, A
Sequence 1, A
Sequence 2, A
Sequence 1,
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Sequence 1,
Sequence 11,
Sequence 6,
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/pubpaa/USO6_PUBCONB.pep:
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:
/cgn2_6/ptodata/1/pubpaa/USO7_PUBCONB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_PUBCONB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_PUBCONB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_PUBCONB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_NEW PEP:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_rub.rcr./cgn2_6/ptodata/1/pubpaa/MS06_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/MS06_PUBCOMB.pep:*/can2_6/ptodata/1/pubpaa/MS06_PUBCOMB.pep:*//mubpaa/WS07_NEW_PUB.pep:
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
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              5.1.4_p5_4578
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-796-294-10

US-09-822-827-946

US-09-965-896-6

US-09-907-402-1

US-09-97-100-11

US-09-874-138-6

US-09-874-238-6
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US-10-183-992-8
US-09-895-793-947
US-09-822-827-947
US-10-183-992-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-895-793-946
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-909-348-1
                                                                                                                                                                                                                                                                    349150 seqs, 92025710 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
               GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
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50
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Match 1
                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
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us-09-909-348-2.rapb

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Sequence 6, Application US/09963896
Patent No. US2002102385A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Guedler, Karl J.
Corley, Wall C.
TILLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
                                                  Sequence 946, Application US/09822827

Batent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICANION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SOT UN 0 946
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 10; Length 261;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/963,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/397,558 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-Sep-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CERRONE, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (650) 855
(650) 855
(650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: (650) 855-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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80.0%;
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-822-827-946
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Best Local Similarity
Matches 8; Conserv
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                                                US-09-822-827-946
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US-09-963-896-6
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TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Anglogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
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US-09-796-294-10
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    Indels
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TITLE OF INVENTION: Extracellular Serine Protease
FILE REFERENCE: D6020CIP3
CURRENT APPLICATION NUMBER: US/09/796,294
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/618,259
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 72
  Mismatches
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Pred. No.
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PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21
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Publication No. US20030012792A1
GENERAL INFORMATION:
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Patent No. US20020037581A1
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Best Local Similarity 80.0%;
Matches 8; Conservative
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 80.0
Matches 8; Conservative
  Conservative
                                                                                                                                                                                                                                                                APPLICANT: Holaday, John W.
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US-10-131-241-62
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LENGTH: 261
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LENGTH: 261
Matches
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                                                          2; Indels
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APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffer
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND
TITLE OF INVENTION: USES FOR IT
FILE REFERENCE: 09011-002003
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Pred. No. 3.3;
                        Pred. No. 1.9;
0; Mismatches
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PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR PLICATION NUMBER: 60/042,678
PRIOR PLICING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PASTSEQ for Windows Version 4.0
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Pred. No. 3
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                                                                                                                                                                                                                                                                                   US-05-874-198-6; Sequence 6, Application US/09874198; Patent No. US20020082208A1
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Patent No. US20020082209A1
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                     80.08;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                     Best Local; Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo saptens
US-09-874-198-6
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US-09-874-238-6
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TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: Compositions and Anglogenesis Using Cancer Markers
FILE REFERENCE: 05213-0343 43170-261379
CURRENT APPLICATION NUMBER: US/09/907,402
CURRENT FILING DATE: 1200-07-17
PRIOR PRILICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1999-06-31
PRIOR FILING DATE: 1999-06-31
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Version 3.1
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| Patent No. US20020099189A1
| GENERAL INFORMATION:
| APPLICANT: SAVITEKK, Kinneret et al.
| TILLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
| FILLE REFERENCE: 2786-0156P
| CURRENT APPLICATION NUMBER: US/09/755,100
| PRIOR APPLICATION NUMBER: UI 128587
| PRIOR PILING DATE: 1999-02-18
| PRIOR PLING DATE: 1999-04-14
| PRIOR PLICATION NUMBER: IL 129439
| PRIOR PLICATION NUMBER: IL 131363
| PRIOR PLICATION NUMBER: IL 131363
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1.3;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-09-963-896-6
                                                                                                                                            Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09907402
Patent No. US20020137668A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
                                                                                                                                            94.0%;
80.0%;
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80.0%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 375
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Matches 8; Conservative
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US-09-755-100-11
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; ORGANISM: Homo sapiens
US-09-907-402-1
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Best Local Similarity
Matches 8; Conserv
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US-09-755-100-11
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US-09-907-402-1
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ALPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER FILE REFERENCE: 2101.21.534C2
CURRENT TILING DATE: 2001-06-29
CURRENT FILING DATE: 2001-06-29
SOFTWARE: FastSEQ for Windows Version 3.0
SQUID NO 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                  Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 947, Application US/09822827 Patent No. US20020081680A1
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Publication No. US20030054432A1
GENERAL INFORMATION:
                                                                              Hepler, William T.
Henderson, Robert A
                                                                                                                                               McNeill, Patricia D
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80.0%;
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80.0%;
                                                                ceiky, Yasir A.W
    Carter, Darrick
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                           John
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US-09-895-793-947
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US-09-822-827-947
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TITLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
FILE REFERENCE: 02877.00008

CURRENT APPLICATION NUMBER: US. 10/10/183, 992

CURRENT FILING DATE: 2002-06-28

PRIOR PEPLICATION NUMBER: US 60/310,125

PRIOR FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENAMORE OF SEQ ID NOS: 80
                                                     APPLICANT: Chen, Lin
APPLICANT: Chen, Lin
APPLICANT: Pepe, Michael
TITLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
FILE REFERENCE: 02877,00008
CURRENT INLING DATE: 2002-66-28
PRIOR APPLICATION NUMBER: US 60/310,125
PRIOR APPLICATION NUMBER: US 60/310,125
PRIOR FILING DATE: 2001-06-28
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10183992
Publication No. US20030054432A1
GENERAL INFORMATION:
Sequence 4, Application US/10183992
Publication No. US20030054432A1
                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Tachypleudus tridentata
US-10-183-992-4
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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962 CSGDSGGPLV 971
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                                      GENERAL INFORMATION
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US-09-895-793-947
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LENGTH: 1019
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APPLICANT: Crowther, Roger S.
APPLICANT: Standors, David J.
APPLICANT: Standors, David J.
APPLICANT: Standors, David J.
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES
FILE REFERENCE: 3033.1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT APPLICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
NUMBER OF SED ID NOS: 6
SOFTWARE: FESTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                              Score 47; DB 9; Length 1083; Pred. No. 5.1; 0; Mismatches 2; Indels
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Pred. No. 0.089;
0; Mismatches 2; Indels
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; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-1
FILE REFERENCE: 02877.00008

CURRENT APPLICATION NUMBER: US/10/183,992

CURRENT FILING DATE: 2002-66-28

FRIOR APPLICATION NUMBER: US 60/310,125

PRIOR FILING DATE: 2001-06-28

NUMBER: OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 1083
                                                                                                                                                                                                                    : TYPE: PRT ; ORGANISM: Carcinoscorplus rotundicauda US-10-183-992-6
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; Sequence 1, Application US/10050692
; Publication No. US20020182205Al
; GENERAL INPORMATION:
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LENGTH: 10
TYPE: PR:
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Search completed: May 12, 2003, 15:59:09 Job time: 20.4 secs

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94.0%; Score 47; DB 2; Length 254; 80.0%; Pred. No. 0.36; 1ve 0; Mismatches 2; Indels
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S39047
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kallikrein – mouse
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                                                                                                            May 12, 2003, 15:33:02; Search time 11.4 Seconds (without alignments) 84.328 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
               GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
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154763
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1: pir1:*
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Match 1
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Maximum DB
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chymotrypsin-like proteinase (EC 3.4.21.-) precursor - california red abalone chymotrypsin-like proteinase (EC 3.4.21.-) precursor - california red abalone)
C; Species: Hallotis rufescens (California red abalone)
C; Date: (O'-Apr-1994 #sequence_revision 19-May-1994 #text_change 22-Jun-1999
C; Accession: 633585; 832750
R; Groppe, J.C.; Morse, D.E.
Arch. Bloothew. Blophys. 305, 159-169, 1993
A; Title: Molluscan chymotrypsin-like protease: structure, localization, and substrate A; Reference number: 835585; MUID: 93343624; PMID: 8342947
A; Recidues: 12-24 <GRO.
A; Residues: 1-234 <GRO.
A; Residues: 1-234 <GRO.
C; Superfamily: trypsin homology
C; Reywords: hydrolase; Intestine; serine proteinase; zymogen
F; 1-23/Domain: aignal sequence #status predicted <SIG>F; 23-254/Product: chymotrypsin-like proteinase #status predicted <MAT>F; 24-251/Domain: trypsin homology <TRY>F; 24-251/Domain: trypsin homology <TRYPSIN trypsin homology <TRYPS
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-May-1997
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-May-1997
C;Accession: PG1235; PG1236
B;Title: Presence of a serine protease in the complement activating component of the A;Reference number: PG1235; MUID: 93176166; PMID: 8439319
A;Reference number: PG1235
A;Molecule type: mRNA
A;Residues: 1-251 GAR>
A;Rocession: PG1236
A;Molecule type: protein
A;Residues: 1-181,122-135;155-173;182-201 CTA2>
C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto C;Reywords: hydrolase; serine proteinase
F;1-243/Domain: trypsin homology <TRV>
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Pred. No. 0.35;
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Gaps

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Cross references: EMEL:U17040; NID:9595945; PIDN:AAA56764.1; PID:9595946
Monne, M.; Croce, C.M.; Yu, H.; Diamandis, E.P.
nncer Res. 54, 6344-6347, 1994
Title: Molecular characterization of prostate-specific antigen messenger RNA expres
Reference number: 152712; MUID:95079406; PMID:7527295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M21895; NID:9189523; PIDN:AAAS9995.1; PID:9189524
A;Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 5-210,'WYLLTELTMPA',223,'PMVLHGSLV',233,'WRGGV' <R13>
A;Cross-references: GB:M21896; NID:g189525; PIDN:AAA59996.1; PID:g189526
A;Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residu
A;Accession: B31567
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A.Title: Complex formation between protein C inhibitor and prostate-specific antigen
A.Reference number: S41212; MUID:94164172; PMID:7509746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 5-164, 'CTPGPDGAAGSPDAWV' <R14>
A; Residues: 5-164, 'CTPGPDGAAGSPDAWV' <R14>
A; Residues: 5-164, 'CTPGPDGAAGSPDAWV' <R14>
A; Rotes: the authors translated the codon GGC for residue 28 as Arg, TGG for residue A; Schaller, J.; Aktyama, K.; Tsuda, R.; Hara, M.; Martl, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
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A; Residues: 25-261 <SC2>
R; Watt, K.W.K.; Lee, P.J.; M'Timkulu, T.; Chan, W.P.; Loor, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 3166-3170, 1986
A; Title: Human prostate-specific antigen: structural and functional similarity with A; Reference number: A23937; MUD:86205857; PMID:2422647
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1r. J. Blochem. 170, 111.120, 1987
1ritle: Isolation, characterization and amino-acid sequence of gamma-seminoprotein, Reference number: S00232; MUID:88082806; PMID:3691515
                                                                                                                                                    A;Residues: 5-261 <LU2>
R;Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, Blochem. Blophys. Res. Commun. 155, 181-188, 1988
A;Itle: Molecular cloning and characterization of novel prostate antigen cDNA's. A;Reference number: A90144; MUID:88326297; PMID:2458104
A;Accession: C31567
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A;Residues: 'PQAYHLHPESCVT',1-176 <RES>
A;Cross references: GB:S75755; NID:g861469; PIDN:AAD14185.1; PID:g4261885
R;Christensson, A.; Lilja, H.
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A; Residues: 25-93, T', 95-164, 'HL', 166, 'YDQM', 169-174, 'Q', 176-261 <WAT>
R; Moreno, J.M.
Babmitted to the EMBL Data Library, November 1994
A; Reference number: G07735
A; Accession: G01551
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Residues: 25-30,'X',32-49 <CHR>
Comment: This enzyme preferentially cleaves after tyrosine residues.
A; Reference number: A26757; MUID:87190978; PMID:2436946
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A; Introns: 16/1; 69/2; 165/1; 210/3
C; Superfamily: trypsin; trypsin homology
C; Eywords: 19/2coprotein; hydrolase; prostate; F; 1-17/Domain: signal sequence #status predicted
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A; Residues: 5-261 <RI2>
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Residues: 1-261 <MOR>
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                                                                                                    A; Molecule type: mRNA A; Residues: 5-261 <LU
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Digby, M.; Zhang, X.Y.; Richards, R.I.
Cleic Acids Res. 17, 2137, 1989
Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallik
Reference number: S03604; MUID:89183632; PMID:2467258
Accession: S03604
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Lochem. Blophys. Res. Commun. 160, 903-910, 1989
Title: CDNA coding for the entire human prostate specific antigen shows high homologie
Reference number: A32546; MUID:89246551; PMID:2470373
                                                                                                                                                                                                                                                                                                                                                                                                 semenogelase (EC 3.4.21.77) precursor [validated] - human
N;Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostat
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M;Utile: Sequence of a cDNA clone encompassing the complete mature human prostate specif
A;Reference number: S02239; MUID:88289366; PMID:2456523
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Title: Characterization of the gene for prostate-specific antigen, a human glandular
Reference number: A32423; MUID:89302090; PMID:2472789
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Residues: 1-72,'T',74-85,'I',87-174,'P',176-183,'Q',185-259,'D',261 <HEN>
Cross-references: GB:M26663
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llobeck, H.G.; Combridato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
ileic Acids Res. 17, 3981, 1989
ittle: Genomic sequence of human prostate specific antigen (PSA).
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Michoeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
bmitted to the EMBL Data Library, May 1989
Reference number: S05468
Accession: S05468
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Cross-references: EMBL:X07730
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Cross-references: GB:M24543
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FEBS Lett. 214, 317-322, 1987
                                                                                                         CSGDSGGPLV 217
                                               1 CXGDSGGPXV 10
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lesidues: 1-261 <KL1>
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Residues: 1-29 <KL2>
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Residues: 17-63,'T',
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C. Genetics:
C. Ge
                              154763
Ra-reactive factor (EC 3.4.21.-) 1 precursor - human
N.Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
N.Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C.Stato, 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
R.Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A.Title: Molecular characterization of a novel serine protease involved in activation
A.Reference number: 154763; MUID:94289349; PMID:8018603
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N;Alternate names: coagulation-complement factor C; Limulus factor C
N;Alternate names: coagulation complement factor C; Limulus factor C light chain peptid
C;Species: Tachypleus tridentatus
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 08-Dec-2000
C;Accession: A38738; B38738; S00105
R;Muta, T.; Miyata, M
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Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the Cls family of complement proteins found in a bactericida
A;Reference number: JNO883; MUID:94059062; PMID:8240317
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A; Residues: 1-234, 'E', 236-284, 'G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699 <TAK>
A; Cross-references: DDBJ:DJ7525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A; Experimental source: liver
C; Comment: This is a serum bactericidal factor that activates complement C4 and C2
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Pred. No. 0.92;
0; Mismatches 2; Indels
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A;Molecule type: mRNA
A;Residues: 1-699 <SAT>
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Matches 8; Conserv
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C;Comment: This protein is localized in the sperm acrosome and is released during the ac
C;Superfamily: trypsin homology
C;ReyWords: hydrolase; serine proteinase
F;71-310/Domain: trypsin homology <TRX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   testicular serine proteinase (EC 3.4.21.-) TESP2 - mouse
N;Alternate names: TESP2
N;Alternate names: TESP2
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: JE0105
R;Kohno, N.; Yamaqata, K.; Yamada, S.; Kashiwabara, S.; Sakai, Y.; Baba, T.
Biochem. Blophys. Res. Commun. 245, 658-665, 1998
A;Title: Two novel testicular serine proteases, TESP1 and TESP2, are present in the mous A;Reference number: JE0104; MUID:98249770; PMID:9588171
A;Accession: JE0105
A;Accession: JE0105
A;Residues: 1-366 <KOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Semenogelase (EC 3.4.21.77) precursor - rhesus macaque
N;Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: 835711; 834239
R;Gauthier, E.R.; Chapdelaine, P.; Tremblay, R.R.; Dube, J.Y.
A;Title: Characterization of rhesus monkey prostate specific antigen cDNA.
A;Reference number: 835711; MUID:9336542; PMID:7689340
A;Accession: 835711
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A; Residues: 1.261 <GAU>
A; Residues: 1.261 <GAU>
A; Residues: 1.261 <GAU>
A; Cross-references: EMBL:X73560; NID:g311843; PIDN:CAA51957.1; PID:g311844
C; Comment: This enzyme preferentially cleaves after tyrosine residues.
C; Superfamily: trypsin; trypsin homology residue; serine proteinase
C; Reywords: glycoprotein; hydrolase; prostate; serine proteinase
F; 1-17/Domain: signal sequence *status predicted <SIG>
F; 18-24/Domain: stopeptide *status predicted <ARO>
F; 25-261/Product: semenoglase *status predicted <AMT>
F; 25-253/Domain: trypsin homology <TRY>
F; 55, 120, 213/Active site: His, Asp, Ser *status predicted
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80.0%; Pred. No. 0.36;
ive 0; Mismatches 2; Indels
                                                                                          Length 261;
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F;65,120,213/Active site: His, Asp, Ser #status predicted
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Pred. No. 0.5;
0; Mismatches
                                                                                          DB 1;
                                                                                                                                            0.36;
                                                                                          Score 47; DB 1
Pred. No. 0.36;
0; Mismatches
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80.0%;
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Best Local Similarity 80.0۰
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Best Local Similarity 80.0
Matches 8; Conservative
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262 CAGDSGGPLV 271
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Best Local Similarity
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C;Accession: 152972
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Baxter, J.D.; Shine, J.
R;Nordeen, S.K.; Mason, A.J.; Richards, R.I.; Rich
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N;Alternate names: pancreatic elastase II [misidentification]
G;Species: Sus scrofa domestica (domestic pig)
C;Species: O5-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A23473
R;Vered, M.; GertLar, A.; Burstein, Y.
Int. J. Pept. Protein Res. 27, 183-190, 1986
A;Reference number: A23473; MUID:86194934; PMID:3634756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elastase (EC 3.4.21.-) 2B - horse (fragments)
C;Species: Equus caballus (domestic horse)
C;Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule-type: mRNA
A;Molecule-type: mRNA
A;Mossules: 1-66 CRES>
A;Cross-references: GB:K01654; NID:g198490; PIDN:AAA39346.1; PID:g198491
C;Superfamily: trypsin; trypsin homology
F;1-58/Domain: trypsin homology (fragment) <TRX>
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R; Dubin, A.; Potempa, J.; Travis, J.
Blochem. J. 300, 401-406, 1994
A; Title: Structural and functional characterization of eA; Reference number: S44461; MUID: 94271153; PMID: 7516152
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Pred. No. 0.15;
1; Mismatches
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A; Residues: 1.31; 32-56; 57-73 < DUB>
C; Superfamally: trypsin; trypsin homology
C; Reywords: hydrolase; serine proteinase
F; 1-73/Domain: trypsin homology (fragments) < TRY>
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70.0%;
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Best Local Similarity 70.00
7; Conservative
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A;Molecule type: protein
A;Residues: 1-126 <VER>
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Matches
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"Residues: 'S',27-39,'S',41,'T',43-54,'E';691-782;950-977 <TOK>
"Residues: 'S',27-39,'S',41,'T',43-54,'E';691-782;950-977 <TOK>
"Superfaulty: complement factor C, C-type lectin homology; complement factor H repeat
"S'Reywords: alternative splicing; glycoprotein; hemolymph coagulation; hydrolase; serine
"1-25/Domain: signal sequence #status predicted <51G-
"1-25/Domain: signal sequence #status predicted <51G-
"1-25/Domain: complement factor C heavy chain #status experimental <HCH>
"1-25/Domain: complement factor H repeat homology <FR01>
F:109-754/Domain: complement factor H repeat homology <FR02>
F:260-321/Domain: complement factor H repeat homology <FR03>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6-564/Domain: C-type lectin homology <LCH>
6-574/Domain: complement factor H repeat homology <FH04>
6-674/Domain: complement factor H repeat homology #status atypical <FH05>
1-762/Product: coagulation factor C light chain peptide A *status experimental <PPA>
3-1019/Product: coagulation factor C light chain peptide B *status experimental <PPA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: PS0049
Yun, Y.; Davis, R.L.
Jl. Cell. Biol. 9, 692-700, 1989
Title: Levels of RNA from a family of putative serine protease genes are reduced in Dr. Reference number: JS0260; MUID:89219063; PMID:2469005
Accession: PS0049
                                                                           R;Tokunaga, F.; Miyata, T.; Nakamura, T.; Morita, T.; Kuma, K.I.; Miyata, T.; Iwanaga, Eur. J. Blochem. 167, 405-416, 1987
A;Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor C) of horseshoe is a novel type of serine protease.
A;Reference number: S00105; WUID:88004461; PMID:3308457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - fruit fly (Drosophila melanogaster) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:523,534,624,912/Alinding site: carbohydrate (Asn) (covalent) #status predicted F:767/Blinding site: carbohydrate (Asn) (covalent) #status experimental F:809,865,966/Active site: His, Asp, Ser #status predicted
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Date: 07-Jun-1990 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Experimental source: strain dnc mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
F; 1-53/Domain: trypsin homology (fragment) <TRY>
F; 30/Binding site: substrate (Val) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2;
Pred. No. 1.3;
0; Mismatches
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1-466,616,'DN',619-620,'A',622 <MU2>
erences: GB:D90272
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80.0%; Pred. No.
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C;Species: Mus musculus (house mouse)
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80.0%;
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Best Local Similarity
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Matches 8; Conserv
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0; Mismatches
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Pred. No. 0
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80.0%;
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80.0%;
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Best Local Similarity 80.07
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                    A; Molecule type: DNA
A; Residues: 1-161 <RES>
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Job time: 11.4 secs
A; Accession: I48158
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                                                                                                                                   C; Species: Mus musculus (house mouse)
C; Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jun-2000
C; Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jun-2000
C; Accession: A00939
R;Richards, R.I.; Catanzaro, D.F.; Mason, A.J.; Morris, B.J.; Baxter, J.D.; Shine, J. J. B.J. Chem. 257, 2758-2761, 1982
A;Title: Mouse glandular kallikrein genes. Nucleotide sequence of cloned cDNA coding for A; Reference number: A00939; MUID:82142394; PMID:6174512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Murakawa, M.; Okamura, T.; Kamura, T.; Kurolwa, M.; Halaud, E., ....., ....., Eur. J. Haematol. 52, 162-168, 1994
A.Title: Analysis of the partial nucleotide sequences and deduced primary structures of A.Reference number: 146196; MUD:94222160; PMID:8168596
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C;Accession: I48158
T; Kamura, T; Kurolwa, M; Harada, M; Niho, Y.
Eur. J Hematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of A;Reference number: 146196; MUID:94222160; PMID:8168596
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(S.Uperfamilly: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan
F;1-161/Domain: trypsin homology (fragment) -TRRY
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A; Experimental source: Quakenbush inbred strain
C; Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
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C. Keywords: hydrolase; saliva; serine proteinase; submandibular gland
F:1-141/Domain: trypsin homology (fragment) <TRY>
F:8.101/Active site: Asp. Ser #status predicted
F:8.0107,72-86,97-122/Disulfide bonds: #status predicted
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Pred. No. 0.35;
0; Mismatches 2; Indels
                                                                                                           N; Alternate names: glandular kallikrein; kininogenin
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80.0%;
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Best Local Similarity 70.0.0
... 7; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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97 CAGDSGGPLI 106
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A; Residues: 1-161 <RES>
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Length 191;

DB 2; 0.41;

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A;Cross-references: GB:D21216; NID:g415304; PIDN:BAA04757.1; PID:g455393 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu F;1-161/Domain: trypsin homology (fragment) <TRY>
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C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Os-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-May-2000
C.Accession: S54115
R.Nicolas, N.
Submitted to the EMBL Data Library, April 1995
A.Recession: S54115
A.Status: preliminary
A.Molecule 'type: mRNA
A.Coross-references: EMBL:Z49058; NID:g773264; FIDN:CAA88844.1; PID:g773265
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                                                                                                                                                                                                                                                                                                     Score 46; DB 2;
Pred. No. 0.35;
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model	May 12, 2003, 15:32:07; Search time 5.8 Seconds (Without alignments) 71.511 Million cell updates/sec
	OM protei	Run on:

US-09-909-348-2 50 1 CXGDSGGPXV 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	P52905 drosophila			_		_		P28175 tachypleus	_	m	capra	Q28412 felis silve	. Q28380 equus cabal	Q28506 macaca mula	P35043 lucilia cup	P00768 vespa orien	P00769	P24664	P00764	P35032	P00761 sus scrofa	Q9bz13	P35033 salmo			Q91041 gadus morhu	P35031	P00760	P19799 xeno	092876	P70059 xeno	P00766 bos taurus
SUMMARIES		TRYI DROME	CTRL_HALRU	KLK3_HUMAN	KLK3 MACMU	CRAR_HUMAN	CRAR_MOUSE	LFC_CARRO	LFC_TACTR	EL2B_HORSE	PRTC_CANFA	PRIC_CAPHI	PRTC_FELCA	PRTC_HORSE	PRTC_MACMU	TRY3_LUCCU	CTR2_VESOR	CTR2_VESCR	TRYP_SACER	TRYP_SQUAC	TRY2_SALSA	TRYP_PIG	TRYD_HUMAN	TRY3_SALSA	TRY5_AEDAE	TRY1_GADMO	TRYX_GADMO	TRY1_SALSA	TRY1_BOVIN	TRY1_XENLA	KLK6_HUMAN	TRY2_XENLA	CTRA BOVIN
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CTRB_GADMO GILX_HELHO TRY1_CANFA TRY1_RAT TRY2_MOUSE TRY2_RAT	TRY1_HUMAN TRY2_CANFA TRY2_HUMAN TRY3_RAT TRY3_RAT KLKC_HUMAN
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ALIGNMENTS

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01-ARR-1988 (Rel. 07, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prostate specific antigen precursor (EC 3.4.21.77) (PSA) (Gamma-seminoprotein) (Kallikrein 3) (Semenogelase) (Seminin) (P-30 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Prostate;

MEDILINE-89183632; PubMed-2467258;

D19by M.R., Zhang X.Y., Richard R.I.;

"Human prostate specific antigen (PSA) gene: structure and linkage to the Kallikrein-like gene, hGK-l.";

Nucleic Acids Res. 17:2137-2137(1989).
                                         SUBGINIT: MONOMER.
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE DISTAL QUARTER OF THE INTESTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHYMOTRYPSIN-LIKE SERINE PROTEINASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
           ENZYME REGULATION: ACTIVATED BY AN AUTOCATALYTIC MECHANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIRONS; SULLALL,
MIRONS; SULLALL,
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Fram; PR00089; trypsin; 1.
PRINTS; PR00020; Tryp_SPG; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS500134; TRYPSIN_BIS; 1.
PROSITE; PS00135; TRYPSIN_BIS; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen.
SIGNAL.

PROSITE: PS00135; TRYPSIN_SER; 1.
Pydrolase; Serine protease; Glycoprotein; Signal; Zymogen.
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                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
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27250 MW;
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PIR, S32750; S32750.
HSSP; P00763; 1DPO.
MEROPS; S01.121;
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SEQUENCE
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                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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           Zheng L.,
Smith H.O.,
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                                                                               The genome sequence of Drosophila melanogaster.";
Science 287.2185-2195(2000)
-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-1- SUBCELLUIAR LOCATION: Extracellular.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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"Molluscan chymotrypsin-like protease: structure, localization, and substrate specificity.";
Arch. Blochem. Blophys. 305:159-169(1993).
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SIMILARITY).
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FROSITE; PS50240; TRYPESIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_ER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Zymogen; Signal; Multigene family.

POTENTIAL.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
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Hallotidae; Hallotis.
NCBI_TaxID-6454;
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 252;
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Pred. No. 0.14;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
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MEDLINE-93343624; PubMed-8342947;
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80.0%;
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EMBL; AE003826; AAF58655.1;
HSSP; P00763; 1DPO.
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  SEQUENCE OF 1-176 FROM N.A.
MEDLINE-95079406; PubMed-7527295;
Monne M., Croce C.M., Yu H., Diamandis E.P.;
"Molecular characterization of prostate-specific antigen messenger RNA
                                                                                                                                                                                                                                                                                                                       TISSUE-Prostate;
MEDLINE-89165891; PubMed-2466464;
Riegman P.H.J., Vlletstra R.J., van der Korput J.A.G.M., Romijn J.C.,
                                                                                                         "Characterization of the gene for prostate-specific antigen, a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence of a cDNA clone encompassing the complete mature human prostate specific antigen (PSA) and an unspliced leader sequence."; Nucleic Acids Res. 16:6226-6226(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                              Monne M.M., Moreno J.M., Mele C.M., Mulholland G.M., Gomella L.G.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                              MEDLINE-89246551; PubMed-2470373;

Heattu P., Vihko P.;

FONA coding for the entire human prostate specific antigen shows

high homologies to the human tissue kallikrein genes.";

Biochem. Biophys. Res. Commun. 160:903-910(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-20510030; PubMed-11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                "Characterization of the prostate-specific antigen gene: a novel human kallikrein-like gene."; Blochem. Biophys. Res. Commun. 159:95-102(1989).
SEQUENCE FROM N.A.
MEDLINE-89282407; Pubmed-2471958;
Klobeck H.-G., Combriato G., Schulz P., Arbusow V., Fittler F.;
"Genomic sequence of human prostate specific antigen (PSA).";
Nucleic Acids Res. 17:3981-3981(1989).
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MEDLINE-88289366; PubMed-2456523;
Schulz P., Stucka R., Feldmann H., Combriato G., Klobeck H.-G.,
                                                                                                                                                                                           "Molecular cloning of human prostate specific antigen cDNA."; FEBS Lett. 214:317-322(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                             lochem. Biophys. Res. Commun. 161:1151-1159(1989).
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SEQUENCE OF 25-261.
MEDLINE-86205857; PubMed-2422647;
                                                                         TISSUE-Leukocyte;
MEDLINE-89302090; PubMed-2472789;
                                                                                                                                                                      MEDLINE-87190978; PubMed-2436946;
Lundwall A., Lilja H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer Res. 54:6344-6347(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in breast tumors
                                                                                                                    glandular kallikrein.
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                                                                                               Lundwall A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-55218633; PubMed-7535613;
Villoutreix B.O., Getzoff E.D., Griffin J.H.;
"A structural model for the prostate disease marker, human prostate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD-STRUCTURE MODELING.
MEDLINE-99427950; PubMed-9751643;
COOMDS G.S., Bergstrom R.C., Pellequer J.L., Baker S.I., Navre M.,
Smith M.M., Tainer J.A., Madison E.L., Corey D.R.;
"Substrate specificity of prostate-specific antigen (PSA).";
Chem. Biol. 5:477-488(1998).
-i- FUNCTION: PRESUMABLY HYDROLYZE THE HIGH MOLECULAR MASS SEMINAL VESICLE PROTEIN THUS LEADING TO THE LIQUEFACTION OF THE SEMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prints, Pro0089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SMO07020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Antigen; Zymogen; Signal;
                                                                                                                                                                                                                        MEDLINE-88082806; PubMed-3691515; Schaller J., Akiyama K., Tsuda R., Hara M., Marti T., Rickli E.E.; Schaller J., Akiyama K., Tsuda R., Hara M., Marti T., Rickli E.E.; Isolation, characterization and amino-acid sequence of gamma-seminoprotein, a glycoprotein from human seminal plasma."; Eur. J. Biochem. 170:111-120(1987).
Watt K.W.K., Lee P.J., M'Timkulu T., Chan W.P., Loor R.; "Human prostate-specific antigen: structural and functional similarity with serine proteases."; Proc. Natl. Acad. Sci. U.S.A. 83:3166-3170(1986).
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InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specific antigen.";
Protein Sci. 3:2033-2044(1994).
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BC005307; AAH05307.1:
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X05332; CAA28947.1;
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Genew; HGNC:6364; KLK3.
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PDB; 1PFA; 26-JAN-95.
PDB; 2PSA; 16-MAR-99.
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                                                                                                                                                                                              SEQUENCE OF 25-261.
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Hydrolase; Serine protease; Glycoprotein; Antigen; Zymogen; Signal
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PP00089; trypsin. 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp_SPC; 1.
PROSITE; PS0040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_ISS; 1.
PROSITE; PS00135; TRYPSIN_ISS; 1.
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Best Local Similarity 80.vv,
8; Conservative
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261
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261 AA;
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
         ACTIVATION PEPTIDE.
PROSTATE SPECIFIC ANTIGEN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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16-CCT-2001 (Rel. 40, Last annotation update)
Prostate specific antigen precursor (EC 3.4.21.35) (PSA) (Gamma-seminoprotein) (Kallikrein 3).
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H -> T (IN REF. 12

V -> M (IN REF. 11

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80.0%;
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PIR; S34239; S34239.
PIR; S35711; S35711.
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Matches 8; Conservative
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261 AA;
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2; Indels

Pred. No. 0.1

Score 47;

N-LINKED (GLCNAC. . .) (POTENTIAL). 8525B14B15967E5C CRC64;

DB 1; Length 261;

(BY SIMILARITY). (BY SIMILARITY). (BY SIMILARITY).

ACTIVATION PEPTIDE

POTENTIAL

PROSTATE SPECIFIC ANTIGEN.
CHARGE RELAY SYSTEM (BY SIM)
CHARGE RELAY SYSTEM (BY SIM)
CHARGE RELAY SYSTEM (BY SIM)
BY SIMILARITY.

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CRAR_HUMAN STANDARD; PRT; 699 AA.
P48740; 095570; GUPF09;
01-FEB-1996 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-OCT-2011 (Rel. 40, Last annotation update)
16-OCT-2011 (Rel. 41, Last 
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MEDLINE-94289349; PubMed-8018603;
MEDLINE-94289349; PubMed-8018603;
Sato T., Matsushita M., Fujita T.;
"Molecular characterization of a novel serine protease involved in activation of the complement system by mannose-binding protein.";
Int. Immunol. 6:665-669(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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MEDLINE-94059062; PubMed-8240317;
Takada F., Takayama Y., Hatsuse H., Kawakami M.;
Takada F., Takayama Y., Hatsuse H., Kawakami M.;
A new member of the Cls family of complement proteins found in bactericidal factor, Ra reactive factor, in human serum.";
Biochem. Biophys. Res. Commun. 196:1003-1009(1993).
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"Exon structure of the gene encoding the human mannose-binding protein-associated serine protease light chain: comparison with complement Clr and Cls genes.";
Int. Immunol. 8:1355-1358(1996).
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MEDLINE-97079701; PubMed-8921412;
CRAR HUMAN

ID CRAR_HIGH

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DT 116-007-

DT 15-007-

DE (ECS 3.40

DE (Annual 1.00

COX MARMAN 1.11

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. pathway; Serine protease; Protease;
Repeat; Signal; EGF-like domain; Hydroxylation.
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EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
CUB 2.
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SUSHI 2.
SERINE PROTEASE.
CHARGE RELAX SYSTEM (BY SIMILARITY).
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80.0%; Pred. No. 0.37;
.tve 0; Mismatches 2; Indels
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29 KDA CHAIN OF P100 (P29).
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 InterPro; IPR001254; Ser_protease_fry.
InterPro; IPR000436; Sushi_SCR_CCP.
                     Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF000431; CBP; 2.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM0014; CBP; 2.
SMART; SM0019; EGF; 1.
SMART; SM0019; EGF. 1.
PMART; SM0019; EGF. 1.
PROSITE; PS00100; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; CGF. 2; 1.
PROSITE; PS01180; EGF. CA; 1.
PROSITE; PS01181; EGF. CA; 1.
PROSITE; PS01187; EGF. CA; 1.
PROSITE; PS01187; EGF. CA; 1.
PROSITE; PS01187; EGF. CA; 1.
PROSITE; PS01184; EGF. CA; 1.
PROSITE; PS01185; TRYPSIN_SER; 1.
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Matches 8; Conservative
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699 AA;
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CRAR_MOUSE
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB010822; BAA34864.1; JOINED.
AB010813; BAA34864.1; JOINED.
AB010815; BAA34864.1; JOINED.
AB010815; BAA34864.1; JOINED.
AB010815; BAA34864.1; JOINED.
AB010817; BAA34864.1; JOINED.
AB010819; BAA34864.1; JOINED.
AB010819; BAA34864.1; JOINED.
AB010820; BAA34864.1; JOINED.
AB010821; BAA34864.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
JOINED.
JOINED.
[4]
SEQUENCE FROM N.A.
MEDLINE-99402590; Pubmed-10475605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB007603; BAA89206.1; JOINED
AB007604; BAA89206.1; JOINED
AB007605; BAA89206.1; JOINED
AB007606; BAA89206.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB007617; BAA89206.1; -. AB007602; BAA89206.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB007614; BAA89206.1; JOINED EMBL; AB007615; BAA89206.1; JOINED EMBL; AB007616; BAA89206.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR000152; Asx_hydroxyl.
InterPro: IPR001859; CUB_domain.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR000561; EGF-like.
InterPro: IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D17525; BAA04477.1; -. EMBL; D28593; BAA05928.1; -. EMBL; D61695; BAA34864.1; -.
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MEROPS;
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SUSHI 2.
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SMART; SM00020; TIYP_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF_Z; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00137; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SRE, 1.
PROSITE; PS00135; TRYPSIN_SRE, 1.
Hydrolase; Complement pathway; Serin
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MEDLINE-95268506; PubMed-7538401;
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80.0%;
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Best Local Similarity 80.00,
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704 AA;
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                                                                                                                                                                                                                                        Glycoprotein;
SIGNAL
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026422;
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CARBOHYD
SEQUENCE
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        SOTHER THE TEST STATES S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOCKERN. BLODMYS. Res. COMMUN. 190:681-687(1993).

- 1- FUNCTION: COMPONENT OF THE BACTERICIDAL RA-REACTIVE FACTOR RARF WHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED BY CERTAIN ENTERCHAELTS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE C4 COMPONENT BY CLEATING THE C4 COMPONENTS. IT ACTIVATING COMPONENT.

- 1- SUBJUNT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT.

- 1- SUBJUNT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT.

- CRARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGH CHAIN (29)

- 1- INKED BY A DISULPIDE BOND.

- 1- TISSUE SPECIFICITY: LIVER.

- 1- DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO CIR AND CIS.

- 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

- 1- SIMILARITY: CONTAINS 2 USB DOMAINS.

- 1- SIMILARITY: CONTAINS 2 USB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-BALLS-C; TISSUE-Liver;
MEDLINE-94179811; Pubmed-8133044;
Takayama Y., Takada F., Takahashi A., Kawakami M.;
"A.100-kDa protein in the C4-activating component of Ra-reactive
factor is a new serine protease having module organization similar to
cir and cis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-93176166; Pubwed-8439319;
Takahashi A., Takayama Y., Hatsuse H., Kawakami M.;
Presence of a serine protease in the complement-activating component of the complement-dependent bactericidal factor, RaRF, in mouse
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precurso (EC 3.4.21.-) (Ra-reactive factor serine protease pl00) (RaRF)
(Mannan-binding lectin serine protease 1).
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     704 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; F. MEROPS; S01.198; -. MEROPS; S01.198; -. InterPro; IPR000152; Asx_hydroxyl. InterPro; IPR000859; CUB_domain. -- Tro; IPR000859; CUB_domain. -- Tro; IPR000859; CUB_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001314; Chymotrypsin.
IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunol. 152:2308-2316(1994).
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Pfam; PF00089; trypsin; 1.
Pfam; PF00431; CUB; 2.
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  STANDARD;
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SMART; SM00042; CUB; 2.
                                                                                                                                                                                                                                              Mus musculus (Mouse)
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Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lisulus clotting factor C precursor (EC 3.4.21.84) (FC).
Carcinoscorplus rotundicanda (Southeast Asian horseshee crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
pplement pathway; Serine protease; Protease;
Sushi; Repeat; Signal; EGF-like domain; Hydroxylation.
                                                                                                                             70 KDA CHAIN OF P100 (P70).
29 KDA CHAIN OF P100 (P29).
CUB 1.
EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
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"Molecular cloning and sequence analysis of factor C cDNA from the Singapore horseshoe crab, Carcinoscorpius rotundicauda.";
Mol. Mar. Biol. Blotechhol. 4:90-103(1995).
                                                                                                                                                                                                                                                                                                                                                 RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                              COMPLEMENT-ACTIVATING COMPONENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                            RA-REACTIVE FACTOR.
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N-LINKED (GLCNAC.
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FUNCTION: THIS ENZYME IS CLOSELY ASSOCIATED WITH AN ENDOTOXIN-SENSITIVE HEMOLYMPH COAGULATION SYSTEM WHICH MAY PLAY IMPORTANT ROLES IN BOTH HEMOSTASIS AND HOST DEFENSE MECHANISMS. ITS ACTIVE FORM CATALIZES THE ACTIVATION OF FACTOR B. CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-|-Ser-104 and 124-IIe-|-I1e-125 bonds in Limulus clotting factor B to form activated factor B. Cleavage of Pro-Arg-|-Xaa bonds in synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAVY CHAIN.
LIGHT CHAIN.
                                                                                                                        -!- ENZYME REGULATION: ACTIVATED BY GRAM-NEGATIVE BACTERIAL IPPOPOLYSACCHARIDES AND CHYMOTRYPSIN (BY SIMILARITY).
-!- SUBUNIT: HETERPROIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULETIE BOND (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 LCCL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
SUBSTRATE (BY SIMILARITY).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A CHAIN.
B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Serine protease; Signal; Lectin; Hemolymph clotting; Glycoprotein; Cell adhesion; EGF-like domain; Sushi; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIMULUS CLOTTING FACTOR C.
LIMULUS CLOTTING FACTOR C, H
LIMULUS CLOTTING FACTOR C, L
LIMULUS CLOTTING FACTOR C, A
LIMULUS CLOTTING FACTOR C, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; SOL 1219; InterPro; SOL 1219; InterPro; IPR001014; Chymotrypsin.
InterPro; IPR0010561; EGF-1ike.
InterPro; IPR001043; LCCLL_dom.
InterPro; IPR0010254; Ser_protease_Try.
InterPro; IPR0010354; Ser_protease_Try.
InterPro; IPR0010354; Ser_protease_Try.
Pfam; PF000099; Ltypsin; 1.
Pfam; PF000099; Ltypsin; 1.
Pfam; PF000099; Ltypsin; 1.
PRNTS; PR007021; CHYMOTRYPSIN.
SWART; SW00031; CHYPSIN; 1.
SWART; SW00031; CEF; 5.
SWART; SW00031; CEF; 1.
SWART; SW00001; TEF; 1.
SWART; SW000021; TEF; 1.
PROSITE; PS00012; TYPE_LECTIN_1; PROSITE; PS000124; CTYPE_LECTIN_2; 1.
PROSITE; PS00136; CEF_1; 1.
PROSITE; PS00134; TRYPSIN_LON; 1.
PROSITE; PS00134; TRYPSIN_LON; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
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SUSHI 4.
SUSHI 5.
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                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
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SUSHI 2.
SUSHI 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S77063; AAB34361.1; -
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690
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762
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137
137
195
254
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01-077-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation)
15-JUN-2002 (Rel. 41, Last annotation)
15-JUN-2002 (Rel. 41, Last annotation)
16-JUN-2002 (Rel. 41, Last annotation)

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--- ENZIME REGULATION: ACTIVATED BY GRAM-NEGATIVE BACTERIAL
LIPOPOLYSACCHARIDES AND CHYMOTRYPSIN.
--- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
                                                                                                                                                                                                                                                                                      (POTENTIAL)
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-i- SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
-i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 LCCL DOMAIN.
BY SIMILARITY.
BY SIM
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Pred. No. 0.54;
0; Mismatches
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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P28175;
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Q28278;
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P37358;
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LIGHT CHAIN.
A CHAIN.
B CHAIN.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
LITIWIG -> IDNVTAT (IN SHORT ISOFORM)
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
SUBSTRATE (BY SIMILARITY).
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PROSITE; PS01080; LCCL; 1.
PROSITE; PS50040; TRYPSIN_LDOM; 1.
PROSITE; PS00134; TRYPSIN_LSER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Signal; Alternative splicing; Lectin; Hemolymph clotting; Glycoprotein; Cell adhesion; EGF-like domain; SignAL.

SIGNAL
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Pred. No. 0.54;
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LIMULUS CLOTTING FACTOR C, ILIMULUS CLOTTING FACTOR C, LIMULUS CLOTTING FACTOR C, B LIMULUS CLOTTING FACTOR C, B EGF-LIKE.
SUSHI 1.
SUSHI 1.
SUSHI 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 5BC2864C6715289B CRC64;
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BY
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C_TYPE_LECTIN_2; 1.
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SUSHI 4.
SUSHI 5.
                                                                                                                                                                                                                                                                                       InterPro; IPR001254; Ser_protease_fry.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF_1; 1.
EGF_2; FALSE_NEG.
LCCL; 1.
                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                 LCCL_dom.
Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                            PR00722; CHYMOTRYPSIN.
M00032; CCP; 5.
M00034; CLECT; 1.
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80.0%;
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EMBL; D90271; BAA14315.1;
EMBL; D90272; BAA14316.1;
                                                                                                                                                                                                                              InterPro; IPR004043;
InterPro; IPR001304;
                                                                                                                HSSP; P00763; 1DPO.
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PROSITE; PS50041;
                                                                                                                                           MEROPS; S01.219;
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SEQUENCE FROM N.A.

MEDLINE=94318474; PubMed=8043441;

Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;

"A comparative study of partial primary structures of the catalytic region of mammallan protein C.";

Br. J. Haematol. 86:590-600(1994).

-I. FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                               TISSUE-Neutrophils;
MEDLINE-94271153; PubMed-7516152;
Dubin A., Potempa J., Travis J.;
"Structural and functional characterization of elastases from horse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNC-1092 (Rel. 41, Last annotation update)
15-UNC-2002 (Rel. 41, Last annotation update)
15-UNC-2002 (Rel. 41, Last annotation update)
(Autoprothrombin IIA)
(Anticoagulant protein C (Blood coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                               neutrophils.";
Biochem. 7. 300:401-406(1994).
-1- FUNCTION: MAY BE INVOLVED IN THE DEGRADATION OF CONNECTIVE
-1- SIMILARITY: BELONG DISEASE.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
BIR; 544462; 544462.
HSSP; P00766; 1GCD.
                                         01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
Neutrophil elastase 2B (EC 3.4.21.-) (Proteinase 2B) (Fragments).
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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AFFB0B330DB69041 CRC64;
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73 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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InterPro; IPR01254; Ser_protease_Iry.
PROSITE; PS500134; TRYPSIN_DOM; PARTIAL.
PROSITE; PS00134; TRYPSIN_IRS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease NON_CONS 31 32 NON_CONS 56 57
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Best Local Similarity 80.(
Matches 8; Conservative
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Gaps

; 0

2; Indels

0; Mismatches

Similarity 80.0 8; Conservative

Best Local Matches

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MEROPS; S01.218;
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ACT_SITE
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REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FACE WAS A PUDMED-8043441;
MEDLINE-94318474; PUDMED-8043441;
MALTAKAWA M., OKEMUTA T., Kemura T., Kurolwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
415-UN-2002 (Rel. 41, Last annotation update)
41tamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                          -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                        PREMI; PRO0089; Trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00104; TRYPSIN_DOW; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 1; Length 157;
Pred. No. 0.13;
0; Mismatches 2; Indels
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                                                  -i- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                             17262 MW; E8B1BACF49220DFB CRC64;
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BY SIMILARITY.
BY SIMILARITY.
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80.0%;
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157 AA;
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Q28315;
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"A comparative study of partial primary structures of the catalytic region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-! FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA.
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALITIC ACTIVITY: Degradation of blood coagulation factors Va
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation in IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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CHARGE RELAY SYSTEM
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Pred. No. 0.13;
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SWART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_EER; 1.
                                                                                                                                                                                                                                                                              InterPro, IPR001254; Ser_protease_Try.
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80.0%;
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Best Local Similarity
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PRTC_MACMU
Q28506;
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DISULFID
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Br. J. Haematol. 86:590-600(1994).
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Murakawa M., Okamura T., Kamura T., Kurolwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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                                                                                                                                                                                                                          Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
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CHARGE RELAY SYSTEM
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Pred. No. 0.13
0; Mismatches
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Pfam; PF00089; trypsin; 1.
SWART; SW00020; Tryp_SPS; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER: 1.
  email to license@isb-sib.ch).
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Pfam; PF00089; trypsin; 1.
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80.0%;
                                      EMBL; D43750; BAA07807.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CEGDSGGPMV 130
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Best Local Similarity
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SEQUENCE
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DTW-2002 (Rel. 41, Last annotation update)
15-JUM-2002 (Rel. 41, Last annotation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJNE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSTTE; PS50240; TRYPSIN_DOM; 1.
PROSTTE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSTTE; PS00135; TRYPSIN_SER; 1.
PROSTTE; PS00135; TRYPSIN_SER; 1.
NON_TER
                                                                                                Hydrolase
                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 1; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                  BFAA6EA045C3C580 CRC64;
                                                                                                     Glycoprotein; Serine protease;
                                                                                                                                                     CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
SMART; SM00020; TTYP_SPC; 1.
PROSITE: PSSO430; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                  17200 MW;
                                                                                                                                                                                                                                                                                                                                                                                  92.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D43754; BAA07811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                     26
125
110
149
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157 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXGDSGGPXV 10
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96
121
                                                                                                     Blood coagulati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     noved. Usage by and for commercial
(See http://www.lsb-s1b.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           veen the Swiss Institute of Bioinformatics and the EMBL outstati
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
26160BlaFF80FICD CRC64;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Musconorpha; Oestroidea; Calliphoridae; Lucilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                     Score 46; DB 1; Length 161;
Pred. No. 0.13;
0; Mismatches 2; Indels
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larity 80.0%; Pred. No. 0.13;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                       27D78F185B2FCC69 CRC64;
  CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  )1-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
hrypsin alpha-3 (EC 3.4.21.4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (sor send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Extracellular
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PROSITE: PS5040; TRYPSIN_DON; 1.
PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE: PS00135; TRYPSIN_SER; 1.
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  26 CJ
129 CJ
114 BJ
153 BJ
17 N
82 N
161 NW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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80.0%;
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Best Local Similarity 80.00
المحقق المحتفظ المحتف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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82
161
161 AA;
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Matches 8; Conserv
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CARBOHYD
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SEQUENCE
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TRY3_LUCCU
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115 CQGDSGGPLV 124
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Search completed: May 12, 2003, 15:36:38 Job time : 6.8 secs

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Gaps

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Query Match
Best Local Similarity
Matches 8; Conserv
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098dll rhizobium l
099gC drosophila
018458 heterodera
016126 boltenia vi
09998 drosophila
095up4 etcmoxys ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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Q9vrd1
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                             671580 segs, 206047115 residues
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                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
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Q98DL1
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria:*
                                                                                                                       US-09-909-348-2
50
1 CXGDSGGPXV 10
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Match Length DB
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sp_human:*
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                                                                                                                       Title:
Perfect score:
                                                                                                                                                                          Scoring table:
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Gaps

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96.0%; Score 48; DB 5; Length 258; 80.0%; Pred. No. 0.29; Live 0; Mismatches 2; Indels ·

Conservative

PERINTS: PR00089; trypsin: 1.

PRINTS: PR00722; CHYMOTRYPSIN.

BMART: SM0020; TRYPSIN.

PROSITE: PS00134; TRYPSIN. DOM: 1.

PROSITE: PS00134; TRYPSIN.HIS; UNKNOWN.1.

Hydrolase; Serine protease; Signal.

SIGNAL 1 16 POTENTIAL.

CHAIN 30 258

TRYPSIN.

SEQUENCE 258 AA; 28070 MW; BDBDFAFECB86866C CRC64;

narours, corrections interpretarion. Interpretarion IPR001314; Chymotrypsin. Interpretarion IPR001254; Ser_protease_Try.

EMBL; X17905; CAA76929.1; -. HSSP; P00763; 1DPO.

MEROPS; S01.113;

Girard C., Jouanin L.; Submitted (ADG-1998) to the EMBL/GenBank/DDBJ databases. -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

SEQUENCE FROM N.A.

TISSUE-GUT;

097398 phaedon coc	ന	O9nh10 agrotis ips	Q9vtv2 drosophila	Q8t9u6 aedes aegyp	O920s2 mus musculu	Ogeogg naemapnysai	O70170 mus musculu	Q9vv14 drosophila				Ogon71 xenonus lae	0911s9 rattus norv	O9vk10 drosophila	Q8t9s1 tachypleus		09v7e5 drosophila	O9gtk6 culex quing			Obrito mus musculu	1	Office Controls January							ate)	inda rej	,	kapoda; Insecta;	otera; Polyphaga; Chrysomelidae:	'sometinge'	
097398 09 va x8	Q9D413	Q9NH10	Q9VTV2	QBT906	092052	09W453	070170	Q9VVI4	09VZT0	Q8T8X4	00111	09PU71	657760	Q9VK10	081951	026423	09V/E5	Q9GTK6	061/52	084TV90	090078	200000	09NR68	090725	ALIGNMENTS		1	PKT; 258 AA.	Created)	Last sequence update)	pase amocaciom apades	(Mustard beetle).	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Endopterygota; Coleoptera; Polyphaga; Maga: Chrysomeloidea: Chrysomelidae:		
94.0 276 5	282	287	0	296	322		366	412	477	483	280	94.0 698 13	701	774	1019	1083	0617		8 6	92.0 73 6	100			138				PRELIMINARI;	(TrEMBLrel.	(TrEMBLrel.	UTSOT	cochleariae (Mustaro	Metazoa; Arthrop	Pterygota; Neoptera; Endopte Cuculiformia: Phytophaga: Cl	ae; Phaedon.	
17 47	. 4	•	▼ .	₹.	4 <	25 47	4	4	4	₹ -		32 . 47	4		4	4	4 -	38 46	4 4	40 40	* 4	43	• •	45 46		RESULT 1	100,000	AC 097399:		DT 01-MAY-1999	DE Trypsin precursor		OC Eukaryota; P			11. RN
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160 CSGDSGGPLV 169
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018458;
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$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\fra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams N.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards N., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D., Wan R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Brandari D., Bollshakov S., Borkova D., Botchan M.R., Buuck J., Brokstein P., Brottler P., Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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EMBL; AP003004; BAB51260.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 152 AA: 16393 MW; E74A9FF9E5567AIF CRC64;
                                                                                                                                                                                                                                                                                                                                               01-OCT-2001 (TTEMBLrel. 18, Last sequence update)
01-MAR-2002 (TTEMBLrel. 20, Last annotation update)
Hypothetical protein mlr4654.
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                                                                                                                                                                                                                                                          152 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                             Mesorhizobium loti.
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                       1 CXGDSGGPXV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG17404 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=381;
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Matches
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RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.W.,

RA Dodoon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fletschmann W.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Helman T.J., Weln P., Ibegwam C.,

RA Harris N.L., Harvey D., Helman T.J., Well M.-H., Ibegwam C.,

RA Jadil M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin Z.,

RA Lasko P., Lei W. McIntosh T.C., McIeod M.P., McPherson D.,

RA Lasko P., Lei W. McIntosh T.C., McIeod W.P., McPherson D.,

RA Markulov G., Malshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mout S.M., Wood M., Murphy B., Nurphy L., Mish D., Parl V., Resse M.G.,

RA Relnert K., Remington K., Stangson M., Skupski M.P., Smith T.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Purl V., Rese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang S., Zhao Q., Zhao Q., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao K., The Genome sequence of Drosophila melanogaster.";

RY Science 287:2185-2195(2000).

C. -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI, ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Sukryota: Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
NCBI_TaxID=51029;
Davies P.,
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MEDLINE-98030247; PubMed-9364965;
Lilley C.J., Urwin P.E., Atkinson H.J., McPherson M.J.;
Characterization of cDNAs encoding serine proteinases from the soybean cyst nematode Heterodera glycines.";
Mol. Blochem. Parasitol. 89:195-207(1997).

EMBL; X13907; CAA74205.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fighese; PEGN0038001; CG17404.
Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_fry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS, PRO0722; CHYMOTREPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DON, 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003695; AAF54763.1; -. HSSP; P00766; 1CHG.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine proteinase precursor. SP-II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypsin;
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cheata; Hexapoda; Insecta; Diptera; Brachycera; Muscomorpha;

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Eukaryota; Metazoa; Arthropoda; Tracheata;
Pteryyota; Neoptera; Endopterygota; Diptere
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                               STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 CSGDSGGPLV 203
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                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
095UP4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The Molecular Evolution of the Vertebrate Trypsinogens.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                  94.0%; Score 47; DB 5; Length 247; 80.0%; Pred. No. 0.43; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.0%; Score 47; DB 5; Length 248; 80.0%; Pred. No. 0.44;
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                                                                                                                      POTENTIAL.
SERINE PROTEINASE.
; 3A2B5B2B3BB77222 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 248 TRYPSIN 1.
248 AA; 25872 MW; AC606B8998413305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Boltenia.
NCBL_TaxID-63515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VQ98 PRELIMINARY; PRT; 248 AA.
Q9VQ98; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG10882 protein.
CG17239.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
HSSP; P00763; 1DPO.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SWART; SW00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF011897; AAB69653.1; -. HSSP; P00763; IDPO.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMARY; SM00020; Tryp_SPc; PROSTIR; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease; Signal.
                                                                                                                                                       247 AA; 25586 MW;
                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                             Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           Trypsinogen 1 precursor.
                                                                                                                                                                                                                                                                         201 CSGDSGGPLV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 CQGDSGGPAV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                           1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boltenia villosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roach J.C.;
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                    Query Match
                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                016126
016126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0990998
1D 099
AC 099
DT 011
DT 010
DE CG
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Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Accorder R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Burton G.G., Wortnam J.R., Yandell M.D., Zhang O., Chen L.X., R.A. Brandon R.C., Boyle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A. An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S., Ballew R.M., Cawley S., Burters R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Bortova D., Bolcher A., Chandra I., Abril S.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Abril M.C., Wolf M. Cawley S., Dahlke C., Davenport L.B., Davis P., Abril M. Cawley S., Dong Z., May R.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan Roche S., Dunkov B.C., Dunn P., Abrils M.Y., Evangeliste C.C., Ferriaz C., Ferriaz S., Fleischmann W., Roller A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., Harvey D., Helman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C., Alali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Howler B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Mannel B.E., Lais M. Murch, P. M., Mannel B.E., McIntosh T.C., McLeod M.P., Mosherson D., Manner S. M., Mannel B.E., McIntosh T.C., McLeod M.P., Mosherson D., Manner S. M., Mannel B.E., McIntosh T.C., McLeod M.P., Mosherson D., Manner S. M., Manner S. M
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradiling A.C., Staplecon M., Skupski M.P., Smith T.,
Spradiling A.C., Staplecon M., Skupski M.P., Smith T.,
Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Xe J., Xeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zhao Q., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.0%; Score 47; DB 5; Length 248; 80.0%; Pred. No. 0.44;
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SEQUENCE 248 AA; 26744 MW; 07B0FD663F005807 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003583; AAF51279.1; -. HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00020; Tryp_SPc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 80.0
کیم 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00089; trypsin;
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HSSP: P00763: 1DPO
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   Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Holf R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthman J.R., Richards S., Ashburner M., Pfelffer B.D.,
Amanatides P.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Aman K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxenddale J., Bayfaktaroglu L., Beaaley E.M.,
Ballew R.M., Basu A., Baxenddale J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Buller H., Cadleu E., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Poolson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Rosler C., Gabriellan A.E., Garg N.S., Glabart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heilman T.J., Hernandez J.R., Heush C.,
Alaris N.L., Havey D., Heilman T.J., Weil M.-H., Ibegwam C.,
Alalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
                                                                                                  Stomoxys calcitrans (Stable fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;

Muscoidea; Muscidae; Stomoxys.

NCBL_TaxID=35570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                   Pamilton J.V., Munks R.J.L., Lehane S.M., Lehane M.J.;

*Association of intestinal Defensin with a Novel Serine Protease in Submitted of Sucking Fly Somoxys calcitrans.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AV044834; AAK98781.1;

InterPro; IPR001284; Ser_protease_Try.

Pran; Pr00089; trypsin, 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNRNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                94.0%; Score 47; DB 5; Length 254;
80.0%; Pred. No. 0.45;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                       Hydrolase; Protease; Serine protease.
SEQUENCE 254 Aa; 27521 MW; 99AAE8B1481FA439 CRC64;
                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AA
 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
 PRELIMINARY;
                                                                        Serine protease Ssp3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 CRGDSGGPAV 215
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXGDSGGPXV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (Tr. CG6580 protein.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Q95UP4
Q95UP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09VRS8
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Matches
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B. W. McIncoh T.C., Moris J., McDherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.K., Nalson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Patled J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Stden Fffamos I., Simpson M., Stwopki N. Suith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Weinstrock G.M., Weissenbach J.,
RA Then S.M., Woodage T., Weinstrock G.M., Rasson M. S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Myers E.W., Rubin G. M., Venter J.C.;
RA Glbbs R.A., Myers E.W., Rubin G. M., Venter J.C.;
Schence 287:2185-2195(2000).
LINERALIYE BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,

Pteryota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,

Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28373 MW; 13249A284038F4F9 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flyase; FBGN03566; CG6580.
InterPo; IPR001314; Chymctrypsin.
InterPo; IPR001314; Chymctrypsin.
InterPo; IPR001254; Scr_procease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PHOGOSIE; PS00135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003564; AAF50712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 101-JUN-2002 (TrEMBLrel. 21, 12ERF protein (RE66795p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
        RA de Pablos B.; Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangedlista C.C., Ferriara C., Ferriara S., Feleischmann W.,
RA Fosler C., Gabriellan A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Hehnan T.J., Hernandez J.K., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Led Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Led Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLedd M.D., Mosherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yell, Yell R.R.F., Zhong F.N., Zhong W., Zhao G., Zhao Q., Zheng X.,
RA The Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.0%; Score 47; DB 5; Length 259; 80.0%; Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SMO0020; TIYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
HYDYCHASS; SETIME PROFERSER; 28078 MW; 49D5EB6E37A9D4DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0011834; Ser6.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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EMBL; AE003569; AAF50872.1; -.
EMBL; AX089642; AAL90380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; CHYMOTRYPSIN.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                             "The genome sequence of Dro
Science 287:2185-2195(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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Q9VRD1
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Adams W.D. Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
A brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pétélfére B.D.,
R. Ballew R.M., Baxue M. H.-J., Andrews-Franckoch C., Baldwin D.,
Ballaw R.M., Baxue M. Barendale J., Bayraktarolu L., Bassley E.M.,
R. Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Burtis R.C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Durkov B.C., Dunkov B.C.,
B. Bothows B., Calcher A., Davan B., Harris M.,
R. Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,
R. Gong F., Gorrell J.H., Gu Z., Kannison J.A., Kecthum K.A.,
Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
Adalal M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Mortet B., McIntex B., Warthy D.M., Nelson D.L.,
Randon D.R., Nelson K.A., Nixon K., Musskern D.R., Parl W., Wang X.,
Randon D.R., Nelson R.A., Nixon K., Wundy D.M., Nelson D.K.,
Randon D.R., Wassacman D.A., Weilstonder J., Wang S., Yuo Q.A,
R. Williams S.M., Woodage T., Shapson M., Strong R., Shen H.,
R. Weiller R., Spradling A.C., Stapletcor R., Weilstenber B.C., Stabletcor G. Druck G., Who M., McInter B., Roder R., Shong S., Bolson R., Scheel R., Spradling A.C., Stab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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PROSITE; PS00134; TRYPSIN_HIS; 1.
HQTCOLBAE; SETINE PICTORENE.
SEQUENCE 260 AA; 27860 WW; 0933B34BF20A7675 CRC64;
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Pred. No. 0.46;
0; Mismatches
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InterPro; IRR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                           MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY.
EMBL; AE003569; AAF50871.1; -.
EMBL; AY095196; AAM12289.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.0%;
80.0%;
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Science 287:2185-2195(2000)
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 287:2185-2195(2000).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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                                       1 CXGDSGGPXV 10
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"Isolation and cloning of Ser4, a gene encoding a trypsin-like serine protease in Drosophila melanogaster.";
Blochim. Blophys. Acta 1395:141-144(1998).
EMBL: AF006639; AdC14351.1;
HSSP; P20231; IAAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease SER4 precursor.
SER4 OR CG8867.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Petergota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                               Gaps
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                                                                                           Score 47; DB 5; Length 262;
Pred. No. 0.46;
0; Mismatches 2; Indels
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1 21 POTENTIAL.
CHAIN 37 265 ACTIVE SERINE PROTEASE SER4.
SEQUENCE 265 AA; 28950 MW; 551A92CDE2E28BC8 CRC64;
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 262 AA; 28511 MW; 7F0F3F66044082CA CRC64;
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Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flyane; Francisco Serd.
InterPro; IPR001254; Ser_protease_Try..
Pfam; PF00089; tryps.in; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                                                94.08;
                                                                                                                    80.08;
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                                                                     Query Match
Best Local Similarity 80.0.
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                                                                                                                                                                                                                     208 CSGDSGGPLV 217
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                                                                                                                                                                                          1 CXGDSGGPXV 10
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SER4 OR CG8867
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1 CXGDSGGPXV 10
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                                                                                              NCBI_TaxID=7165;
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                            Adams M.D., Celniker S.E., Il P.W., Boxins C.A., Gocayne J.D., Ray Manatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Il P.W., Hoskins R.A., Galle R.F., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Staton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Staton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Staton G.C., Bazdwin D., Balanchoch C., Baldwin D., Ballew R.M., Basu A., Dayler E.G., Helt G., Nelson C.R., Miklos G.L.G., Ballewin D., Ballew R.M., Basu A., Dayler E.G., Helt G., Nelson C.R., Miklos G.L.G., Ballew R.M., Basu A., Baxendala J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Cavler B. V., Berman B.P., Bhandari D., Botchan M.R., Bouk J., Brokstein P. Brottler A., Chandra I., Rery D., Botchan M.R., Deud E., Downes M., Dugan T.C., Dew I., Dietz S.M., Re Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Re Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M., Re Pablos B., Delcher A., Bownes M., Dugan Tocha S., Pleischman W., Burtis N.L., Barvey D., Hernandez J.R., Houck J., Rayler B., Gorrell J.M., Gus T., Gong E., Gorrell J.M., Gus T., Bouck J., Botchin M.S., Gong E., Gorrell J.M., Gus T., Botchin M.S., Martis M.L., Marvey D., Lei Y., Levitsky A.A., Howlind T.J., Hernandez J.R., Rockman D.L., Rak Mout S.M., Wolly B., Murphy L., Muzny D.M., Nalson D.L., Reiner J.M., Mallan N.V., Mobarry C., Morris J., Mosheri A., Rawling A., Musny D.M., Nalson D.L., Ruben G.M., Spier E., Spradling A.C., Persier R., Verlor R., Stude S., Palazzolo M., Pittman G.S., Pen S., Pelascolo J.M., Rayle B.C., Siden-Kianos I., Sinpson M., Stupsky M., Nalson M., Stupsky M., Stupsky M., Wally M., Murphy B., Murphy L., Muzny D.M., Nalson D.L., Rheiner C., Stenics E., Spradling A.C., Turner R., Vender E., Spradling A.C., Turner R., Vender E., Spradling A.C., Turner R., Vender E., Spradling A.C., Stapleton M., Stupsky M., Wally M., Wally M., Murphy M., Murphy M., Murphy M., Murphy M., Murphy 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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PRINTS: PRO0722: CHYMOTRYPSIN.
SMART: SM00205; TYPESTIN.
PROSITE: PS00134; TYPESTIN.DM: 1.
PROSITE: PS00134; TRYPSIN.LHS: 1.
PROSITE: PS00135; TRYPSIN.LHS: 1.
Hydrolase: Serine protease: Serine protease: Serine protease: Serine protease: Serine protease: Serine protease: SERINE PROFESTIN.THS 1.
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Last annotation update)
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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                    MEDLINE-20196006; PubMed-10731132;
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Matches 8; Conservative
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01-FEB-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Serine protease.
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WEDLINE-20196006; Pubbed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., In P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandaell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Maril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ra Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.I., Benos P.V., Berman B.P., Brandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ra Borkova D., Delcher A., Deng Z., Mays A.D., Dew I. D. Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Ra Dodson K., Gongelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Ra Fosler C., Gabriellan A.F., Garrell J.H., Gu Z., Gunn P., Harris M.,
Ra Fosler C., Gabriellan A.F., Gun W., Harris M.,
Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                           SEQUENCE FROM N.A.
SETALINE-3; TISSUE-MIDGUT;
MEDLINE-97075119; PubMed-8917545;
Dimopoulos G.M., Richman A., della Torre A., Kafatos F.C., Louis C.;
Dimopoulos G.M., Richman A., della Torre A., Kafatos F.C., Louis C.;
"Identification and characterization of differentially expressed cDNAs of the vector mosquito, Anopheles gamblae.";
Proc. Natl. Acad. Sci. U.S.A. 93:13066-13071(1996).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE FEMEL; Z69978; CAA9318.1; -.
HSSP; PO0763; IDPO.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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SEQUENCE 268 AA; 29176 MW; 7BEE8462EFIFD8BE CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 5;
Pred. No. 0.47;
0; Mismatches
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INTERPROJ IPRO01314; Chymotrypsin,
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PRO0089; trypsin; I.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; I.
PROSITE; PS00134; TRYPSIN.DOM; I.
PROSITE; PS00135; TRYPSIN.HIS; UNKNOWN_I.
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Martel B., McIntosh T.C., McLeod M.P., Inlang Y., Lin X.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Mosherel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shie B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
Shier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Welisteck E., Wang A.H., Wang X.,
Williams S.M., Woodage T., Worley K.C., Wu D., Xang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
R. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E. George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mingali C.J., Nunco J., Pacleb J., Paragas V., Park Fatel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.0%; Score 47; DB 5; Length 271;
80.0%; Pred. No. 0.48;
ive 0; Mismatches 2; Indels
                                        C., Kravitz S., Kulp D.
                   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.Ä
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPhersk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Serine protease.
SEQUENCE 271 Aa; 29814 MW; 0A410C925CBE8826 CRC64;
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ROSITE; PS50240; TRYPSIN_DOM; 1.

ROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

ROSITE; PS00135; TRYPSIN_SER; 1.
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IPR001254; Ser_protease_Try
089; trypsin; 1.
00722; CHYMOTRYPSIN.
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Best Local Similarity
Matches 8; Conserv
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Search completed: May 12, 2003, 15:38:40 Job time : 24.6 secs

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             2110c
2210c
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ABP48609
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Thrombin peptide d
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Thrombin-induced p
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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AAM50856
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Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteolytically activated thrombin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thronain receptor (MRRA). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide. The derivatives of thrombin peptide which serves as a NPAR agonist.
                                                                                                                                                                                                                                                                                                                                                       therapy; implantation; thrombin peptide; human.
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llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
Pred. No. 7.8e+05;
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                                                                                                                                                                                                  AAE20157 standard; peptide; 4 AA.
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larity 100.0%; P
Conservative 0;
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                                                                                                                                                                                                                                                                                                                       Human thrombin peptide.
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Best Local Similarity
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel ligands which bind to transport molecules, comprising a therapeutic and/or diagnostic agent (A) non-covalently bonded via a linkage cleavable in vivo depending on pH and/or enzymatically with a substance (B) having an association constant KA to a transport molecule of above 10~3 M^-~1, is new. The medicaments are especially useful for the treatment of cancers, autoImmune diseases, acute and chronic inflammation and infections caused by viruses or microorganisms. The diagnostic kits are useful for the detection of the transport molecule and/or its distribution in vivo. The ligands have excellent solubility in the medium at the site of action are easy and inexpensive to covert into adducts, as the interaction with the transport material is physical.
                                                                                                                                                                                                                                                               Gaps
                                                      The sequences given in AAR25311-19 are cyclic peptides which act as contact inhibitors of animal cells. They are resistant to decomposition by hydrolytic enzymes and can be maintained at high lavels of activity for a long period in vivo. The peptides are cyclic and may have 1-16 pref. 1-4 amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transport molecule; ligand; cancer treatment; autoimmune disease; inflammation; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New ligand, comprising therapeutic or diagnostic agent bonded non-covalently with substance having high affinity to transport
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                                                                                                                                                                                                                     Length 4;
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100.0%; Score 21; DB 13;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;
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                  Disclosure; Page 3; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 39; 74pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KTBT-) KTB TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB86859 standard; peptide; 4 AA.
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Query Match

Kratz F;

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Gaps ö

Length 4; Indels

24 - JAN - 2002

Synthetic.

Carney DH,

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The present sequence is that of a thrombin receptor binding domain peptide that is used in a claimed method for promoting cardiac peptide that is used in a claimed method for promoting cardiac tissue repair. The method involves administering an angiogenic thrombin derived peptide. The peptide comparises the present thrombin receptor binding domain together with a scrine esterase conserved sequence (see AAM50857), or preferably a peptide (see AAM50858) which includes both these sequences. The thrombin-derived peptide is administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. It is used in claimed methods of stimulating revascularisation, stimulating vascular occlusion, and inhibiting restencial peptide may be coated onto the catheter.
                                                                                                                                             Promoting cardiac tissue repair, stimulating revascularisation, stimulating vascular endothelial cell proliferation, and inhibiting vascular occlusion by using anglogenic thrombin derivative peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides which are useful
have higher activity than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide(s) comprising arginine-glycine-asparagine and hyaluronic acid - useful as platelet antagonists with higher activity than arginine-glycine-asparagine-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 23;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR24514-8 are platelet antagonists. These peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR24517 standard; Protein; 5 AA
                                                                                                                                                                                                                              Claim 2; Page 19; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clinical effect; antagonist.
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                 (TEXA ) UNIV TEXAS SYSTEM.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP04134096-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR24517;
                                                               Carney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
AAR24517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of stimulating bone growth at a site in a subject in need of osteoinduction. The method involves administering an agonist to stimulate bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoinduction, such as the site in need of a bone graft in a subject, a segmental bone gap, a bone void or a non-union fracture. This sequence represents a thrombin peptide derivative obtained from a serine esterase that can stimulate or activate the non-proteolytically
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stimulating bone growth at a site in a subject in need of osteoinduction, such as a site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombin receptor binding domain; thrombin; revascularisation; vascular occlusion; tissue repair; vulnerary; vasotropic; cardiant; angiogenesis; restenosis; therapy; human.
                                         Thrombin; osteopathic; receptor; agonist; bone growth stimulation; osteoinduction; farm animal; companion animal; laboratory animal; bone graft; segmental bone gap; bone void; non-union fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombin receptor binding domain used for cardiac tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                 Redin WR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 23;
100.0%; Pred. No. 7.8e+05;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 Yang J,
                                                                                                                                                                                                                                                                                                                                                                                 Simmons DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM50856 standard; Peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 22; 27pp; English.
Thrombin peptide derivative #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUL-2001; 2001WO-US21944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2000; 2000US-217583P.
                                                                                                                                                                                                                                                      18-JUL-2001; 2001WO-US22641.
                                                                                                                                                                                                                                                                                              19-JUL-2000; 2000US-219300P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activated thrombin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Crowther RS,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-303796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 A
                                                                                                                                                                     WO200205836-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200204008-A2
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01-MAY-2002

AAM50856;

1 RGDA 4

Matches

Sequence

1 RGDA

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RESULT 5 AAM50856 17-JAN-2002

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Gaps

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Length 4; Indels us-09-909-348-3.rag

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WPI; 2001-226546/23
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            stent placement
                                                                                                                          WO200112656-A1
                                                                                                                                                                                                                              Schmaler AH,
                                                                                                                                                                                     17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibronectin;
                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US4879237-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1989
                                                                                                                                                                                                                                                                                                     activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR04871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PXPXPXXXXXX
    human immunodeficiency virus (HIV) by treating the virus, or its target cell, with a thrombospondin or thrombospondin analogue. Thrombospondin blocks binding of HIV to its cellular receptors. Thrombospondin or its analogues can used to prevent infection by HIV, in both contraceptive and non-contraceptive compositions/devices. They are already known to reduce infectivity of some bacteria and protozoa. The present sequence represents a human thrombospondin-1 type III repeat peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for suppressing infectivity of human immunodeficiency virus (HIV) by treating the virus, or its target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                         Gaps
conventional peptide of Arg-Gly-Asp-Val. These peptides have a clinical effect at a lower dose, dosage is 2.5-5.0 mg/kg/day.
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                                                                                                                                                                                                                                               Human; thrombospondin; HIV; infection; inhibition; chemokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5;
                                                     Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suppressing infectivity of human immune deficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 20;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                   Score 21; DB 13;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                          Human thrombospondin-1 type III repeat peptide.
                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          Nachman RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 33; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB72600 standard; Peptide; 5 AA.
                                                                                                                                                              AAY17781 standard; peptide; 5 AA.
                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                     (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                      98US-0078873.
97US-0066294.
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-370856/31.
                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AA;
                              5 AA;
                                                                                                                                                                                                                                                          contraceptive
                                                                                                                                                                                                                                                                                                           W09926649-A1
                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1998;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                   24-NOV-1998;
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2 RGDA 5
                                                                                                                                                                                                      12-AUG-1999
                                                                                                                                                                                                                                                                                                                               03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         Crombie AR,
                                                                                                      RGDA
                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGDA
                                                                                           RGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                Sequence
                                                                                                                                                                                   AAY17781;
                                                            Best_Loca
Matches
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ID AAB7
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                                                                                                                                            RESULT 7
                                                                                                                                                       AAY17781
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The present invention relates to a method for inhibiting thrombin cartivation in a human cell expressing protease activated receptor 1 (PARI). The method involves using peptides (e.g. the present peptide) that inhibit platelet activation. The method is useful for preventing thrombosis and platelet aggregation. The method can be used for patients with acute coronary syndromes (e.g. cresendo anglan, myccardial infarction) and for individuals who have acute coronary syndromes and receive percutaneous transluminal coronary angioplasty with an artificle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activated receptor 1 (PAR1), comprises contacting mixtures of thrombi
and human cell expressing PAR1, with a peptide that inhibits platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell attachment; cell detachment; fermentation; therapy
                                                                                                                                             Platelet aggragation inhibitor; thrombin activation inhibitor; protease activated receptor 1; PARI; platelet activation inhibitor; thrombosis; acute coronary syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting thrombin activation in human cell expressing
                                                                    Thrombin-induced platelet activator antagonist #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR04871 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 26; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-2000; 2000WO-US40669
09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hasan AAK;
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Gaps

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Indels Length

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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polypencientide (III) encoding (I) or (II); and (S3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                         locally such as in the case of an operation performed in the peritoneal cavity, to prevent adhesions and scar formations locally as in the case of eye operations, for prophylactic inhibiton of E. coll binding to epithelial cells of the urhary tract or intestine, diagnosis and treatment of E. coll related infections, and identification of various pathogenic bacterial strains. The peptide is pref. prepd. by solid phase synthesis.
peptide can be used for eg mobilisation of bone marrow cells; prevention and reversal of attachment of disseminated tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc finger protein; ZFP; DNA binding protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc finger protein related peptide motif SEQ ID NO:289.
                                                                                                                                                                                                         100.0%; Score 21; DB 12; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 37; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       ABP48385 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANG-) SANGAMO BIOSCIENCES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-500284/53.
                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                               6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200242459-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                            1111
2 RGDA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                            1 RGDA
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        ABP48385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu 0;
                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                              Synthetic peptide(s) from fibronectin- used in control of cell attachment
                                                                                                                                                                                                                        This polypeptide mediates the attachment of animal cells to substrates. The substrate (I) is contacted with cells and with a soln. contg. this polypeptide. This attachment can be prevented in addition to detaching the cells from (I) once attached. Applications are in eg fermentation, cell line prepn., diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The peptide, or shorter versions contg. the RGD active site from fibronectin, can be used to prevent and reverse attachment of cells to substrates. This can be used in cell prodn., fermentation, cell line prepn., cell matrix prodn., diagnostics and therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nseq
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                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 21; DB 11; Length 6; 100.0%; Pred. No. 7.8e+05; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide(s) contg. arginine-glycine-aspartic acid sequence to prevent and reverse cell attachment or to promote cell
                                                                                Pierschbacher MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruoslahti EI, Hayman EG, Pierschbacher MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 2..4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell attachment promoting peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 8; 12pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR11506 standard; Protein; 6 AA.
                                                                                                                                                                                             Claim 1; page 10; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87US-0131130.
85US-0738078.
                89us-0738078
                                                (JOLL-) LA JOLLA CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87US-0131130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JOLL-) LA JOLLA CANCER FOU
                                                                              Hayman EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-116404/16.
                                                                                                            WPI; 1990-154405/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibrin; aggregation,
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                         6 AA;
                                                                                                                                                               and detachment
                                                                              Ruoslahti EI,
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24-MAY-1985;
               24-MAY-1989;
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) a target site, comprising a first (FI), a second (F2), and a third (F3) to carry first (FI), a second (F3), a second 
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a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP46191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
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The present invention describes a zinc linyer protein (1) that Juneal Ju
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and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ71214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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The present invention describes a zinc finger protein (1) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, comprising a first (F1), a second (F2), and a third (F3) zinc finger site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I): (2) a polynucleotide (III) encoding (I) or (III); and (S) dealgning (M) (I) involves selecting the F1 zinc finger such that the binds to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, thus designing (I) carget subsites having the nucleotide (II) is useful for recognition of the capacitate and plant engineering. (I), (II) or (III) is useful in the properties and plant engineering. (I), (II) or (III) is useful in the capacitic detection of a subject, and alarget region within a subject, and a subject, and a subject and in assays to determine the
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                                                                                                              Gaps
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Pred. No. 7.8e+05;
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                                       Score 21; DB 23;
Pred. No. 7.8e+05;
Mismatches 0;
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in the exemplification of the present invention
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Matches 4; Conserv
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Search completed: May 12, 2003, 15:36:04 Job time : 12.44 secs	leted: 12.44	May 12, secs	2003,	15:3(. 70.9				

21, Appl 5196510 5196510 5352664 50, Appl

Appl Appl Appli Appli

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Sequence 2, Appli
Sequence 8, Appli
Patent No. 5196510
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
                                                                                                                                                                 Sequence 19,
Sequence 50,
Sequence 50,
Sequence 2, A
Sequence 8, A
                                            Sequence 2
Sequence 2
Patent No.
Patent No.
Sequence 5
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hawley Nelson, Pamela
APPLICANT: Ean, Jianging
APPLICANT: Shih, Poden
APPLICANT: Shih, Poden
APPLICANT: Shifferli, Revin P.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLE OF INVENTION: Transfections
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US.

ZIP: 80303

ZIP: 80303

ZIP: 80303

ZUPERRIBE READALE FORM:
MEDIUW TYPE: RLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,130

FILING DATE: 04-JUN-1996

CLASSIFICATION NUMBER: US 08/477,354

FILING DATE: 07-JUN-1995

ATORNEY/AGENT INFORMATION:
NAME: CAINTHERS: 34,464

REGISTRATION NUMBER: 34,464

REGISTRATION NUMBER: 34,464

REGISTRATION NUMBER: 32-95A

TELEPHONE: (303) 499-8089

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARATERISTICS:
US-08-127-351-21
US-08-480-3678-21
US-08-487-221A-21
US-08-480-370-21
5196510-30
5196510-30
5196510-30
519664-1
US-07-609-716-50
US-08-642-255-19
US-08-475-411A-50
US-08-475-41A-50
US-08-475-41A-50
US-08-475-41A-50
US-08-489-1
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US-08-487-221A-20
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US-08-127-351-20
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not relevant
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STRANDEDNESS: sir
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FRAGMENT TYPE:
US-08-658-130-19
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US-08-658-130-19
      CITY: STATE:
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                                                                                                                                                                 (without alignments)
30.649 Million cell updates/sec
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Sequence 2,
Sequence 32,
Sequence 32,
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Patent No. 5
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                                                                                                                                                May 12, 2003, 15:33:37; Search time 3.84 Seconds
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-139-762A-100
US-09-139-762A-113
US-07-609-716-14
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US-08-482-085B-35
US-08-475-411A-14
US-08-478-029A-14
US-09-444-791A-35
US-08-981-088-4
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US-09-644-600-85
US-07-602-847C-1
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                                                                                                            OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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21
1 RGDA 4
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                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 6; Length 4; 100.0%; Pred. No. 2e+05;
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                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/08723 FILING DATE: 04-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5352664-2
;Petent No. 5352664
; Tetent No. 100 Darrell H.;Glenn, Revin C.
TILLO OF INVENTION: THROMBIN DERIVED POLYPEPTIDES
;COMPOSITIONS AND METHODS FOR USE
                                              E: Greenlee, Winner and Sullivan, 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 3295A WO
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,354
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,201
FILING DATE: 31-OCT-1986
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US-08-232-081B-3
; Sequence 3, Application US/08232081B
                                                                                                                                                                       COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM; PC-DOCUMENTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080.
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 4; Conserv
                                                                                                            STATE: Colorado
                                                                                                                                                                                                                                                                                                             FILING DATE: 04
CLASSIFICATION:
                                                                                  Boulder
                                              ADDRESSEE:
                                                                                                                           COUNTRY:
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      Length 4;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,780A,
FILING DATE: 16-Mar-198
                                                                                                                                                                                                                                                                                                                              SHIH, POJEN
JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
GEBEYEHU, GULLLAT
INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Life Technologies, Inc.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLE OF INVENTION: Transfections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
CITY: BOULDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 4;
illarity 100.0%; Pred. No. 2e+05;
Conservative 0; Mismatches
    Score 21; DB 1;
Pred. No. 2e+05;
                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-039-780A-23
                                                                                                                                                                                                                        Sequence 23, Application US/09039780A
Patent No. 6376248
GENERAL INFORMATION:
APPLICANT: LAWLEY NELSON, PAMELA
LAN, JIANOING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: CURKOWN>
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
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GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303 499-8089)
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
  100.08;
ilarity 100.08;
Conservative 0
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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Best Local Similarity
Matches 4; Conserva
Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF NUMBER OF
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PCT-US96-08723-19
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US-09-039-780A-23
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APPLICANT: Lazarus, Robert A.,
APPLICANT: Seymour, Jana L.
TITLE OF INVENTION: No. 5227469el Platelet Aggregation Inhibitors From The Leec
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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No. 5227469el Platelet Aggregation Inhibitors From The Leec
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Pred. No. 35;
                        Length 9;
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                        100.0%; Score 21; DB 4; 100.0%; Pred. No. 2e+05;
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                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION 135
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION INDER: 07/479,829
FILING DATE: 14-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07602847C Patent No. 5227469
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APPLICANT: Leazurus, Robert A.,
APPLICANT: Seymour, Jana L.
TITLE OF INVENTION: NO. 522746;
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MEDIUM TYPE: 5.25 inch, 360
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 1:
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                      Query Match
Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
Matches 4; Conserv
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US-07-602-847C-1
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                                                                                                            1 RGDA 4
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APPLICAMT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: OVEREXPRESSED in Carcinomas
TITLE OF INVENTION NUMBER: US/09/644,600
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
PRIOR FILING DATE: 1998-02-20
SEQ ID NO 85
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Residues 248-256 of the TADG-15 protein US-09-644-600-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                          SPETWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,081B
                                                      APPLICANT: GOMI, HIDEVOKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NGCHI, HIDSOHI
TITLE OF INVENTION: HUMANIZED B-BIO
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSE:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 2;
Pred. No. 2e+05;
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 85, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEGONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 amino acids
                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                      FALLS CHURCH
Patent No. 5886152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-644-600-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-232-081B-3
                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                        CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: GB 9422534.9
PRIOR APPLICATION DATA:
                                                        FILLING DATE: 10-00-1293
PRIOR APPLICATION DATA:
APPLICATION NOMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STANDENNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
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Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
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20-AUG-1994
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-139-762A-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 1; Length 10; 100.0%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W.
                                                                                                                 COMPUTER: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPREY: USA
ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                       SOFTWARE: patin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/602,847C
FILING DATE: 19901026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-00N-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
                                                                                                                                                                                                                                                       FILING DATE: 1990126
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/479,829
FILING DATE: 14-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 667
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
  : 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;<u>`</u>
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TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                             California
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APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
No. 5770697el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                      NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flehr, Hohbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PELLING DATE: 07-JUN-1995
CLASSIETCATION NUMBER: US/08/477,509B
FILING DATE: 07-JUN-1995
CLASSIETCATION NUMBER: US/08/175,155
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/053,049
FILING DATE: 20-CT-1987
PRIOR APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
FILING DATE: 1900-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 1; 100.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK FELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989 TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35, Application US/08482085B
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Chambers, James
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrari, Franco A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Causey, Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chambers,
                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6018030
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                        94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-477-509B-35
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US-08-482-085B-35
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                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                            Length 10;
                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Sour Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
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                                                                          100.0%; Score 21; DB 3;
100.0%; Pred. No. 35;
ive 0; Mismatches C
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Patent No. 5770697
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Sequence 14, Application US/07609716
Patent No. 5514581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ROALand, Bertram I
REGISTRATION NUMBER: 20015
REFRENCE/DOCKET NUMBER: A-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 14:
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100.0%;
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Crissman, John w
Dorman, Mary A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                              Best_Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-139-762A-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-609-716-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                      1 RGDA 4
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US-07-609-716-14
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COUNTRY:
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APPLICANT:
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APPLICANT:
                                                                              Query Match
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STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ferrati, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,029A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING APPLICATION NUMBER: US 06/927,258
FILING APPLICATION NUMBER: US 06/927,258
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: A-55186-9/RFT/ATK
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION NOMBER: US APPLICATION NOMBER: US APPLICATION NOMBER: US FILING DATE: 09-NOV-1988
             US/08/475,411A
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08478029A Patent No. 6184348 GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity luv...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid.
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ZIP: 94111
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US-08-478-029A-14
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STATE:
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Patent No. 6140072
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/08/482,085B FILING DATE: U7-JUN-1995 CLASSIFICATION: 435
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PatentIn Release #1.0, Version #1.30
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Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION NUMBER: US 08/15,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/175,155
FILING DATE: 190-DEC-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
naupumer: IBM PC compatible
                                                                                                                                                  COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-482-085B-35
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                         San Francisco
                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserva
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SOFTWARE: PatentI
                                                                                                                                                                              OPERATING SYSTEM:
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STRANDEDNESS: si
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Gaps

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: Treaceartin, Richard F.

REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTK

TELEPHONE: 415-391-3249

TELEPHONE: 415-391-3249

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERSTICS:

LENGTH: 11 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: all ami
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Search completed: May 12, 2003, 15:40:39 Job time : 5.84 secs

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RESULT 2
US-10-050-611-1
; Sequence 1, Application US/10050611
; Publication No. US20020187933A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 289, Requence 670, Requence 671, Sequence 672, Sequence 673, Sequence 674, Requence 674, Requence 675, Re
                                                                                                                                                                                               (without alignments)
47.436 Million cell updates/sec
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Sequence 3,
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Sequence 3,
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-911-569-23
US-09-909-348-3
US-09-909-122-3
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US-09-990-186-289
US-09-990-186-671
US-09-990-186-673
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US-09-990-186-673
US-09-990-186-673
US-09-990-186-675
US-09-990-186-675
US-09-990-186-696
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US-09-990-186-1048
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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21
1 RGDA 4
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                                                                                                                                                                    Run on:
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Sequence 2005, Sequence 2007, Sequence 2016, Sequence 2116, Sequence 3169, Sequence 3177, Sequence 3702, Sequence 3702, Sequence 289, Sequence 670, Sequence
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US-09-990-186-1961
US-09-990-186-1990
US-09-990-186-1990
US-09-990-186-1990
US-09-990-186-2007
US-09-990-186-2007
US-09-990-186-2014
US-09-990-186-3169
US-09-990-186-3177
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US-09-989-789-672
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US-09-989-789-674
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US-09-989-789-670
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ALIGNMENTS

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Gaps
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Sequence 3, Application US/10050692

Publication No. US20020182205A1

GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Carney, Darrell H.
APPLICANT: Simmons, David J.
APPLICANT: Simmons, David J.
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: SPEPTIDE DERIVATIVES
FILE REPRENCE: 3093.1002-004
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
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llarity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 4
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
HAWLEY-NELSON, PAMELA
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                                                                                                                                                                                                                                                                                                         ZIP: 80303
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 4; Conservative
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APPLICANT:
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APPLICANT: Crowther, Roger S.
APPLICANT: Stiernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: SIMULATION OF CARTILAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTECLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
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                                       TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED ITILE OF INVENTION: PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4;
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llarity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 0;
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                                                     TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 3033.1000-008
CURRENT APPLICATION NUMBER: US/10/050,611
CURRENT FILING DATE: 2002-01-16
PRIOR PLLING DATE: 2007-01-09
PRIOR PLLING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/217,583
PRIOR FILING DATE: 2000-07-12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 09/909,348
PRIOR FILING DATE: 2001-07-19
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Publication No. US20030069173A1
GENERAL INFORMATION:
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n No. US20020198154A1
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                  Darrell H.
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Stiernberg, Janet
APPLICANT: Bergmann, John
APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin
FILE REFERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
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SCHIEFERLI, KEVIN P.
GEBEYEHU, GULILAT
TILLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                          ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/911,569
FILING DATE: 23-Jul-2001
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENÇE/DOCKET NUMBER: 32-95D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-09-911-569-23
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                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 23:
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APPLICANT: LIU, Q1ang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 289
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE. REFERENCE: 8325-0011.21 / S11-053
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ilarity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.1e+05;
                                                                  100.0%; Score 21; DB 10;
100.0%; Pred. No. 3.1e+05;
tive 0; Mismatches 0;
; OTHER INFORMATION: Peptide fragment of Thrombin US-09-909-122-3
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CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
LENGTH: 7
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5. US20030068675A1
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ORGANISM: Artificial Sequence
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                                                                                                            Conservative
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Publication No.
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROWBIN DERIVED
TITLE OF INVENTION: PEPTIDES
TILE REFERENCE: 3033.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
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TITLE OF INVENTION: Peptide Derivatives
FILE REFERENCE: 3033.1002-001
                                                                                                                                                                      Length 4;
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                                                                                                                                                                  Score 21; DB 10;
Pred. No. 3.1e+05;
; Mismatches 0;
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                                                                                                        ; OTHER INFORMATION: Peptide fragment of Thrombin US-09-909-348-3
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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PRIOR FILIMS DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.0
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PRIOR FILING DATE: 2000-07-19
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ORGANISM: Artificial Sequence
                                               TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Crowther, Roger S.
Simmons, David J.
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APPLICANT: Carney, 1
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZING FINGERS
FILE REFERENCE: 8325-0011.21 / S11-0S3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 674. Application US/09990186
Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: LIU, Qlang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
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; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-674
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; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-673
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                                                                                                                                                               100.0%; Score 21; DB 9; I
ilarity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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                                                    ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 675
LENGTH: 7
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NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.
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Matches 4; Conserva
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                               PYPE: PRT
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                                                                                        APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / 811-053
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILE DATE: 2001-11-20
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.21 / 811-053
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
SOFTWARE: Patentin Vos: 4085
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: example 2FP US-09-990-186-671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-990-186-672
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Pred. No. 3.1e+05;
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CURRENT FILLING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 672, Application US/09990186
Publication No. US20030068675A1
                          Application US/09990186 o. US20030068675A1
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ORGANISM: Artificial Sequence
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Best Local Similarity
US-09-990-186-671; Sequence 671; Ap; Publication No.
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US-09-990-186-673
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Sequence 696, Application US/09990186
Publication No. US20030068675a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.21, S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 696
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence CERATURE: ORGANISM: Artificial Sequence: example ZFP US-09-990-186-696
US-09-990-186-696
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Search completed: May 12, 2003, 15:59:09 Job time: 7.76 secs

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Gaps

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Query Match 100.0%; Score 21; DB 9; Length 7; Best Local Similarity 100.0%; Pred. No. 3.1e+05; Matches 4; Conservative 0; Mismatches 0; Indels

us-09-909-348-3.rpr

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 12, 2003, 15:33:02; Search time 4.56 Seconds (without alignments) 84.328 Million cell updates/sec

US-09-909-348-3 21 1 RGDA 4 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	36K microfibril-as	decorsin - leech (hypothetical prote		~	hypothetical prote	thetical	60s ribosomal prot	trp RNA-binding pr	hypothetical prote	unknown protein en	ydaQ protein - Esc	cytochrome c551 -	conserved hypothet	cell surface glyco	hypothetical prote	probable prophage	hypothetical prote		hypothetical prote	ribosomal protein	ribosomal protein			hypothetical prote		hypothetical prote	e acyl	partial transposas
SUMMARIES	£ £	A34467	A36453	G82812	S70093	S19623	E70535	AG3217	S62570	139905	B90870	G85748	E64884	268677	н82662	168553	E82562	AH0620	E82696	G84240	D83771	A71054	C75089	E82962	S01566	T30673	E75273	F70976	B72538	F90230
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T51207 E97566	AC2787 S14024 C82479	D71832 D64681	B81255 I35719	H75059 D84319	S62816 T03574	C86883 B72621 T37063
99	0 0 0	0 0	M M	0 N	0 N	999
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21	222	21	21	21	212	222
30 31	9 9 9 4 9 2	3 3 3 2	38	39	417	4 4 4 5 4 5

ALIGNMENTS

ABSULT 1 A34467 36K microfibril-associated protein - pig (fragment) C:Species: Sus scrofa domestica (domestic pig) C:Species: Sus scrofa domestica (domestic pig) C:Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Jun-1993 C:Accession: A34467 R:Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Haya J. Biol. Chem. 264, 17437-1744, 1989 A;Title: Isolation and characterization of a new 36-kDa microfibril-associated glycop A;Acteresion: A34467; MuID:90008913; PMID:2793866 A;Accession: A34467 A;Status: preliminary A;Modecule type: protein	A; Residues: 1-19 < KOB> Query Match Query Match Best Local Similarity 100.0%; Score 21; DB 2; Length 19; Best Local Similarity 100.0%; Pred. No. 60; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 RGDA 4 Db 5 RGDA 8
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decorsin - leech (Macrobdella decora)
C;Species: Macrobdella decora
C;Species: Macrobdella decora
C;Date: 08-Mar-1991 \$sequence_revision 08-Mar-1991 \$text_change 30-Sep-1993
C;Accession: A36453
R;Seymour, J.L.; Henzel, W.J.; Nevins, B.; Stults, J.T.; Lazarus, R.A.
J. Biol. Chem. 265, 10143-10147, 1990
A;Title: Decorsin. A potent glycoprotein IIb-IIIa antagonist and platelet aggregation A;Reference number: A36453; MUID:90277628; PMID:2351655
A;Accession: A36453
A;Molecule type: protein
A;Residues: 1-39 <SEY>

ó Gaps ö Query Match
100.0%; Score 21; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels

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1111 31 RGDA 34 g

RESULT 3 682812 hypothetical protein XF0386 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa

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100.0%; Score 21;
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Best Local Similarity 100.

Matches 4; Conservative
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Matches 4; Conserva
                                                                                                                   A; Accession: S19623
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-52 <MAZ>
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24 RGDA 27
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A; Residues: 1-45 <SIN>
A; Molecule type: DNA
A; Residues: 1-45 <SIN>
A; Molecule type: DNA
A; Residues: 1-45 <SIN>
A; Cass.references: GB:AE003890; GB:AE003849; NID:g9105215; PIDN:AAF83196.1; GSPDB:GN001
A; Experimental source: Strain 9a5c
A; Experimental source: Strain 9a5c
B; Simpson, A.J.G.; Relnach, E.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.S.; Bueno, M.S.; Ferrora, T.S.; Carraro, D.M.; Carrer, T. Submitted to GenBank, June 2000
A; Authors: Ferreira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Krieger, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marzuca, S.C.; Franco, M.V.; Martins, E.A.; Nunes, L.R.; Oliveira, M.N.; Madeira, H.M.F.; Marzuca, E.C.; Miyaki, C.Y.; Fodrigues, V.; Rosa, A.J. de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr.V., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Reference number: A59328
A; Re
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C;Species: Amycolatopsis methanolica
C;Species: Amycolatopsis methanolica
C;Date: 15-Feb-1997 $sequence_revision 13-Mar-1997 $text_change 07-May-1999`
C;Accession: 870093
R;Vrijbloed, J.W.; Jelinkova, M.; Hessels, G.I.; Dijkhuizen, L.
A;Vrijbloed, J.W.; Jalinkova, M.; Hessels, G.I.; Dijkhuizen, L.
A;Title: Identification of the minimal replicon of plasmid pMEA300 of the methylotrophid
A;Reference number: 870087; MUID:96154938; PMID:8596458
                    C; Accession: G82812
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Asture 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID: 20365717; PMID: 10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Status: preliminary
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C;Species: Placobdella ornata
C;Species: Placobdella ornata
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S19623
R;Mazur, P.; Henzel, W.J.; Seymour, J.L.; Lazarus, R.A.
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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C,Genetics:
A;Start codon: GTG
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Best Local Similarity 100.
Matches 4; Conservative
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A; Molecule type: DNA
A; Residues: 1-49 <VRI>
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RGDA 26
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C;Species: Mycobacterium tuberculosis (strain H3/KV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uil-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: E70535
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamili, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230
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C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Accession: Ag317
R; Wood, D; W; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
Science 294, 2317-2333, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:295972; GB:AL123456; NID:g3261790; PIDN:CAB09391.1; PID:e31919 A;Experimental source: strain H37Rv C;Genetics:
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Eur. J. Biochem. 202, 1073-1082, 1991
A;Title: Ornatins: potent glycoprotein IIb-IIIa antagonists and platelet aggregation
A;Reference number: S19566; MUID:92111479; PMID:1765068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
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A; Status: prelininary
A; Status: prelininary
A; Molecule type: DNA
A; Residues: 1-68 < KUR>
A; Residues: 1-68 < KUR>
A; Residues: GB: AE008687; PIDN: AAL46157.1; PID:g17743927; GSPDB:GN00188
A; Experimental source: strain C58 (Dupont)
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llarity 100.0%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+02;
11ve 0; Mismatches 0;
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Length 68;

DB 2;

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unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: G85748
R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-79 <STO>
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: E64884
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64884
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                          protein ECs1930 [imported] - Escherichia coli (strain O157:H7, substrain
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C;Genetics:
                                                                                                                                                                   F.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                 C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Accession: B90870
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ilarity 100.0%; Pred. No. 2.4e+02;
Conservative 0; Mismatches 0;
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100.0%; Score 21; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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A; Residues: 1-79 <HAY>
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A;Reference number: Z21801
A;Reference number: Z21801
A;Accession: T38587
A;Status: pre-liminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 1-74 <PE2>
                                                                                                                                                                                                                                                                N'Alternate names: protein SPAC30D11.1
C'Species: Schizosaccharomyces pombe
C'Species: Schizosaccharomyces pombe
C'Species: Schizosaccharomyces pombe
C'Accession: S6270; T38587
R'SPearson, D.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A'Reference number: S62559
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                            Indels
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 21; DB 2; 7
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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A.Map position: 1L
A.Introns: 1/3; 641.
C.Superfamily: rat ribosomal protein L38
C.Keywords: cytosol; protein blosynthesis; ribosome
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36 RGDA 39
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Gaps

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Length 88

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C;Accession: 168553
R;Horn, G.T.; Bugawan, T.L.; Long, C.M.; Manos, M.M.; Erlich, H.A.
Hum. Immunol. 21, 249-263, 1988
A;Tille: Sequence analysis of HLA class II genes from insulin-dependent diabetic indi
A;Reference number: 154290; MUID:88227495; PMID:3372263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M35000; NID:9291960; PIDN:AAA35774.1; PID:9553265 C;Superfamily: class II histocompatibility antigen; immunoglobulin homology C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 04-0ct_1996 #sequence_revision 04-0ct-1996 #text_change 23-Jul-1999
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                                                                                                                                           Score 21; DB 2;
Pred. No. 2.6e+02;
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A;Molecule type: DNA
A;Residues: 1-89 <RES>
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Job time: 7.56 secs
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Matches 4; Conservative
  A, Reference number: A59328
A, Contents: annotation
C, Genetics:
A, Gene: XF1562
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44 RGDA 47
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A; Residues: 1-80 <SAM>
A; Residues: 1-80 <SAM>
A; Experimental source: strain D
C; Superfamenty: cytochrome c6; cytochrome c6 homology
C; Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; oxidative phos F; 1-77/Domain: cytochrome c6 homology <CYC>
F; 10, 13/Binding site: heme (Cys) (covalent) #status predicted
F; 14, 59/Binding site: heme iron (His, Met) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S68677
R; Samyn, B.; de Smet, L.; van Driessche, G.; Meyer, T.E.; Bartsch, R.G.; Cusanovich, M.P. Bur. J. Blochem. 236, 689-696, 1996
A; Title: A high-potential soluble cytochrome c-551 from the purple phototrophic bacteriu A; Reference number: S68677; MUID:96195682; PMID:8612646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: H82662
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A;Cross-references: GB:AE000232; GB:U00096; NID:g1787600; PIDN:AAC74428.1; PID:g1787608;
A;Experimental source: strain K-12, substrain MG1655
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R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Bilones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein XF1562 [imported] - Xylella fastidiosa (strain 9a5c)
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Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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100.0%; Pred. No. 2.4e+02;
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A; Residues: 1-88 <SIM>
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A;Gene: ydaQ
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008542 P50619 Q9h0t7

B3G1_MOUSE IDI_MYCTU EFA4_MOUSE YMAB_BACSU RB17_HUMAN

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PIR; A36453; A36453
PDB; 1DEC; 31-AUG-9
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Best Local Similarity
Matches 4; Conserv
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01-MAY-1992
15-JUL-1999
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                                                                                                                                         112892 seqs, 41476328 residues
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APG1_HUMAN
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R38B_SCHPO
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C551_CHRVI
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RL21_PYRHO
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NEDLINE-94278502; PubMed-8009227;

MEDLINE-94278502; PubMed-8009227;

MEDLINE-94278502; PubMed-8009227;

"Structure of the RGD protein decorain: conserved motif and distinct function in leech proteins that affect blood clotting.";

Science 264:1944-1947(1994).

-I- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GIYCOPROTEIN IIB-IITA COMPLEX. MAY PREVENT BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE OF INGESTED BLOOD.

-I- SIMILARITY: HIGH, TO P.ORNATA ORNATINS.

-I- SIMILARITY: SOME, TO THE DISINTEGRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seymour J.L., Henzel W.J., Nevins B., Stults J.T., Lazarus R.A.; Decorsin. A potent glycoprotein Inb-IIIa antagonist and platelet aggregation inhibitor from the leech Macrobdella decora."; J. Biol. Chem. 265:10143-10147(1990).
                                                                                                                                                                                                                                                                                                          Macrobdella decora (North American leech).
Wakaryota, Metazoa, Annelida; Clitellata; Hirudinida; Hirudinea,
Arynchobdellida; Hirudiniformes; Hirudinidae; Macrobdella.
NCBI_TaxID-6405;
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Pred. No. 48;
Mismatches 0; Indels
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Last annotation update)
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ALIGNMENTS
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llarity 100.08;
Conservative 0;
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    RX MEDLINE-21848401; PubMed-11859360;
RA MEDLINE-21848401; PubMed-11859360;
RA MEDLINE-21848401; PubMed-11859360;
RA Good V., Gailliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Radocks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown C., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Rochies S., Goble A., Hamilan N., Harris D., Hidalpo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A money P., Noules S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Retton J., Simmonds M., Squares R., Squares S., Stevens K.,
Retton S., Simmonds M., Squares R., Squares S., Stevens K.,
Retton J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Rochyard J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Retton J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Rodel C., Fuchs M., Fritzc C., Holzer E., Mosetl D., Hilbert H.,
Rager P., Zimmermann W., Wedder H., Reinhardt R., Purnelle S.,
Radel C., Euchs M., Fritzc C., Holzer E., Moset D., Mottler S.,
Radel D., Calleu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
Radlibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Table G.,
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                                                                                                                                                                 -i- FUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. MAY PREVENT BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE OF
                                                                                                                                                                                                                                -1- SIMILARITY: HIGH, TO THE OTHER P.ORNATA ORNATINS, AND TO M.DECORA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                        MEDLINE-92111479; PubMed-1765068; Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.; Ornatins: potent glycoprotein Inb-IIIa antagonists and platelet aggregation inhibitors from the leech Placobdella ornata."; Eur. J. Biochem. 202:1073-1082(1991).
Placobdella ornata (Turtle leech).
Bukaryota, Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Rhynchobdellida; Glossiphoniidae; Placobdella.
NCBL_TaxID-6415;
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                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 1; Length 52; 100.0%; Pred. No. 64;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
16-S ilbosomal protein Li8-2.
RPL38B OR RPL38 OR SPAC30D11.12.
Schlzosaccharomyces pombe (Fission yeast).
Eukaryota, Fungl; Ascomycota; Schlzosaccharomycetes; Schlzosaccharomycetes; Schlzosaccharomycetae;
                                                                                                                                                                                                                                                                                                                                      Blood coagulation; Platelet; Cell adhesion.
SITE 42 44 CELL ATTACHMENT SITE.
SEQUENCE 52 AA; 5845 MW; BA55CA740BEF4F09 CRC64;
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                                                                                                                                                                                                                                                             -1- SIMILARITY: SOME, TO THE DISINTEGRIN FAMILY.
PIR; S19623; S19623.
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Pfam; PF02088; Ornatin; 1.
PRINTS; PR01184; ORNATIN.
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Best Local Similarity
4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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J. Bacteriol. 177:839-842(1955).
-1- FUNCTION: REQUIRED FOR TRANSCRIPTION ATTENUATION CONTROL IN THE TRAP OPERON. THIS TRANS-ACTING FACTOR SEEMS TO RECOGNIZE A 10 BASES NUCLEOTIDE SEQUENCE IN THE TRP LEADER TRANSCRIPT CAUSING TRANSCRIPTION TERMINATION. BINDS THE LEADER RNA ONLY IN PRESENCE
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerritti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).

-I- MISCELLANEOUS: There are two genes for L38 in S. Pombe.
-I- SIMILARITY: BELONGS TO THE L38E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription attenualion protein mtrB (Tryptophan RNA-binding attenuator protein) (Trp RNA-binding attenuation protein) (TRAP).
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NCBI_TaxID=1408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002675; Ribosomal_L138e.
Pfam; PF01781; Ribosomal_L138e; 1.
ProDom; PD010361; Ribosomal_L138e; 1.
Stbosomal protein; Multigene family.
SEQUENCE 74 AA; 8339 MW; C90D6594DFCB11D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus pumilus (Bacillus mesentericus).
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MEDLINE-95138053; PubMed-7836324;
Hoffman R.J., Gollnick P.;
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Best Local Similarity 100.
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InterPro; IPR001147; Ribosomal_L21e.
Pfam; PF01157; Ribosomal_L21e; 1.
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                                                                                                                                                                                                                                                                                                             STRAIN-GE5 / Orsay;
Heilig R.;
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69 RGDA 72
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074001;
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MEDLINE-96195682; PubMed-8612646;
Samyn B., de Smet L., van Driessche G., Meyer T.E., Bartsch R.G.,
Cusanovich M.A., van Beeumen J.J.;
"A high-potential soluble cytochrome c-551 from the purple
phototrophic bacterium Chromatium vinosum is homologous to cytochrome
c8 from denitrifying pseudomonads.";
Eur. J. Blochem. 235:689-696(1996).
-i- FUNCTION: MONOHEME CYTOCHROME.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                             Chromatium vinosum.
Bacteria: Proteobacteria: gamma subdivision; Chromatiaceae;
Allochromatium.
                                                                       Score 21; DB 1; Length 76;
Pred. No. 93;
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                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COVALENT).
(HEME AXIAL LIGAND).
(HEME AXIAL LIGAND).
         Pfam; PF02081; TrpBP; 1.
PRINTS; PR00687; TRPRNAAP.
Transcritton regulation; RNA-binding.
SEQUENCE 76 AA; 8301 MW; 22184B2351DA151D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EBD30A2815D07F93 CRC64;
                                                                                                                                                                                                                                           01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
1-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome c-551 (C551).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEME (COVALENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1b-OCT-2001 (Rel. 40, Last sequence update)
50s ribosomal protein Lile.
PPL/1B OR PAB0731.
                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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InterPro, IPR003088; Cyt_CI.
InterPro, IPR002324; Cyt_CID.
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00034; cytochrome_c; 1.
PRINTS; PR00606; CYTCHROMECID.
PROSITE; PS00190; CYTOCHROME_C; 1.
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IRON
IRON
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                                                                         100.0%;
100.0%;
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InterPro; IPR000824; TrpBP
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Matches 4; Conser
                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1049;
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                                                                                                                                                   RGDA 61
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P80549;
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Q9UZP1;
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C551_CHRVI
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RL21_PYRAB
                                                                                                  Matches
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SKRDR
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Yamamoto S., Sekine M., Baba S. I., Kosuqi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii O73.";
"Pyrococcus abyssi genome sequence: insights into archaeal chromosome
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                  structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L21E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE L21E FAMILY OF RIBOSOMAL PROTEINS.
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Pred. No. 1.2e+02;
Mismatches 0;
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PROSITE; PS01171; RIBOSOMAL_L21E; 1.
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MEDLINE-98344137; PubMed-9679194;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.("Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human cytomegalovirus encodes a glycoprotein homologous to MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                    Length 97;
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                                           6D5D229DBFBE0E51 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Top. Microbiol. Immunol. 154:125-169(1990).
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Pred. No. 1.2e+02;
Mismatches 0;
                                                                                  Score 21; DB 1; Dred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                       01.AUG-1990 (Rel. 15, Created)
01.AUG-1990 (Rel. 15, Last sequence update)
01.FEB-1991 (Rel. 17, Last annotation update)
Hypothetical protein UL19.
                                                                                                                                                                                                                                                                                                                  98 AA
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(Rel. 39, Last sequence update)
                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytomegalovirus (strain AD169).
                     Ribosomal protein; Complete proteome SEQUENCE 97 AA; 11376 MW; 6D5D22
PROSITE; PS01171; RIBOSOMAL_L21E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y00293; -; NOT_ANNOTATED_CDS.
EMBL; X17403; CAA35418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90269039; PubMed-2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88094735; PubMed-2827039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 100.0%; Si
Similarity 100.0%; P:
4; Conservative 0;
                                                                                100.0%;
                                                                                                 Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               class-I antigens.";
Nature 331:269-272(1988).
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beck S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S01566; S01566.
PIR; S09782; S09782.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 4; Conserv
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Q15772;
30-MAY-2000 (
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|95 RGDA 98
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69 RGDA 72
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P16723:
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                                                                                  Query Match
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APG1_HUMAN
  S W S
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                                                                                                                                                                                                                                                                                                                        Haich C. M., Yoshicum M., Endege W.O., Kho C.-J., Jain M.K.,
Kashiki S., de Los Santos R., Lee W.-S., Perrella M.A., Lee M.-E.;
"AppC.1, a novel gene preferentially expressed in aortic smooth muscle
cells, is down-regulated by vascular injury.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIFFERENTIATION OF ARTERIAL SMOOTH MUSCLE CELLS.

-1- FUNCTION: MAY HAVE A ROLE IN REGULARING THE GROWTH AND DIFFERENTIATION OF ARTERIAL SMOOTH MUSCLE CELLS.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN DIFFERENTIATED ARTERIAL SWOOTH MUSCLE CELLS (ASMC).
-1- DEVELOPMENTAL STAGE: APPEARS: TO BE EXPRESSED ONLY IN HIGHLY DIFFERENTIATED ASMC IN NORMAL VESSEL WALLS AND DOWN REGULARED IN DEDIFFERENTIATED ASMC IN VIVO. IN RESPONSE TO VASCULAR INJURIES ASMC DEDIFFERENTIATE AND CHANGE FROM A QUESCERM AND CONTRACTILE PHENOTYPE TO A PROLIFERRATIC PHENOTYPE. THIS PROLIFERRATION OF VASCULAR SWOTH MUSCLE CELLS IS ONE OF THE MOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eùteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                   Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROMINENT FEATURES OF ARTIOSCLEROSIS.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
10-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Aortic preferentially expressed protein 1 (APEG-1).
15-JUN-2002 (Rel. 41, Last annotation update)
Aortic preferentially expressed protein 1 (APEG-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE-96291890; PubMed-8663449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U57099; AAC50599.1; -. EMBL; BC006346; AAH06346.1; HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
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85 RGDA 88
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Q62407;
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Ribosomal protein; Complete pr
SEQUENCE 116 AA; 13392 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                              HSSP; P56276; 1TLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=85963;
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MEDLINE-96291890; PubMed-8663449;
MEDLINE-96291890; PubMed-8663449;
Hasheh C.-M., Yoshizumi M., Endege W.O., Kho C.-J., Jain M.K.,
Hasheh C.-M., a novel be constanted by vascular by the service and the cells, is down-regulated by vascular injury.";
J. Biol. Chem. 271:17354-17359(1996).

-I FUNCTION: MAY HAVE A ROLE IN REGULATING THE GROWTH AND
DIFFERENTIATION OF ARTERIAL SMOOTH WUSCLE CELLS.

-I SUBCELLULAR LOCATION: Nuclear.

-I SUBCELLULAR LOCATION: Nuclear.

-I TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DIFFERENTIATED ARTERIAL
SMOOTH MUSCLE CELLS (ASMC) IN THE MEDIAL LAYER OF THE AORTA.
                                                                                          MEDLINE-96291890; PubMed-8663449;
Haish C.-M., Yoshizumi M., Endege W.O., Rho C.-J., Jain M.K.,
Rashiki S., de Los Santos R., Lee W.-S., Perrella M.A., Lee M.-E.;
"APEG-1, a novel gene preferentially expressed in acrtic smooth muscle
cells, is down-regulated by vascular injury.";
J. Biol. Chem. 271:17354-17359(1996).
I- FUNCTION: MAY HAVE A ROLE IN REGULATING THE GROWTH AND
DIFFERENTIATION OF ARTERIAL SMOOTH MUSCLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN DIFFERENTIATED
Manmalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P562/0; 1100.

MGD; MGI:109282; Appell.

InterPro; IPR003006; Ig_MRC.

InterPro; IPR003598; Ig_C2.

SMART; SM00407; Ig; 1.

SMART; SM00408; IGc2; 1.

Immunoglobulin domain; Nuclear protein.

DOMAIN

34 95 IG-LIKE DOMAIN.

112 ha: 12665 MW; 5F320C5A41C3D870 CRC64;
                                                                                                                                                                                                                                                                                      ARTERIAL SMOOTH MUSCLE CELLS (ASMC).
-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aortic preferentially expressed protein 1 (APEG-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 AA.
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                        SEQUENCE FROM N.A.
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85 RGDA 88
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                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb-sib.ch).
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MEDLINE-99120557; PubMed-9923682;
Alm R.A. Ling L.-S.L. Moir D.T., King B.L., Brown E.D., Dolg P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Glason R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Nature 397:176-180(1999).
-I- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50S ribosomal protein Li7.
RPLO OR JHP1212.
RPLO OR JHP1212.
Belicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria: epsilon subdivision; Hellcobacter group;
WEAKLY DETECTED IN BRAIN AND TESTIS AND TO A LESSER EXTENT IN ORGANS RICH IN STRIATED MUSCLE OR VISCERAL SMOOTH MUSCLE. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EBC77780E2F2F3A1 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; 19; 1.
SMART; SMO0408; IGc2; 1.
Immunoglobulin domain; Nuclear protein.
DOMAIN 34 95 IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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InterPro; IPR000456; Ribosomal_L17.
Pfam; PF01196; Ribosomal_L17; 1.
ProDom; PD004277; Ribosomal_L17; 1.
TIGRFAMS; TIGR00059; L17; 1.
PROSITE; PS01167; RIBOSOMAL_L17; 1.
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(Rel. 35, Last sequence update) (Rel. 40, Last annotation update)
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                             50S ribosomal protein L17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                             RPLQ OR MPN192 OR MP639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                            Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 RGDA 110
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                                                                                                                                                                                                                                                                                                                                                               pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS8E_HALN1
Q9HPE9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                Tomb J.-F., White O., Kerladge A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pylori.";
Nature 388:539-547(1997).
-1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 1; Length 116; Pred. No. 1.4e+02;
              Length 116;
Score 21; DB 1; Length 1. Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13364 MW; EBD87890E2F2E4B6 CRC64;
                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AA
                                                                                                                                                                                   116 AA
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                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@lsb-sib.ch)
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Pfam: PF01196; Ribosomal_L17; 1.
ProDom: PD004277; Ribosomal_L17; 1.
TIGRFAMs; TIGR00059; L17; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01167; RIBOSOMAL_L17; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97394467; PubMed-9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
RL17_MYCPN STANDARD; I
LO RL17_MYCPN STANDARD; I
C S59547;
DT 01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000633; AAD08335.1; -.
             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0;
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Similarity 100.0%;
4; Conservative 0,
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SEQUENCE 116 AA; 13364 MW
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
                                                                                                                                                                                                                                                                50S ribosomal protein L17. RPLQ OR HP1292.
                                                                                                                                                                                     STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-210;
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                                                                           1 RGDA 4
                                                                                                                                                                                                                  01-NOV-1997
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                                                                                                                                                                                   RL17_HELPY
P56042;
                                                                                                                                                    RESULT 13
RL17_HELPY
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Matches
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                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATC2 29342 / M129;
STRAIN-ATC2 29342 / M129;
HIDDET H., Himmelreich R., Plagens H., Herrmann R.;
Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
"Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Procured Caids Res. 24:4420-4449(1996).
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
NCBI_raxID=2104;
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NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Ballaja N.S., Thorson V., Sbrogna J. Swartzell S., Weir D., Hall J., Dahl T.A., Weiti R., Goo Y.A. Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 21; DB 1; Length 124; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3A627DB7EBF8C62E CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein S8e.
30S Rels OR VMG1668G.
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SEQUENCE 124 AA; 14245 MW; 3A6271
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InterPro; IPR000456; Ribosomal_L17
Pfam, PF01196; Ribosomal_L17; 1.
TIGRPAMS; TIGR00059; L17; 1.
PROSITE; PS01167; RIBOSOMAL_L17; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5-JUN-2002 (Rel. 41, Created)
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Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., "Genome sequence of Halobacterium species NRC-1."; "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 21; DB 1; Length 124; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0307; SBe; 1.
PROSITE; PS01193; RIBOSOWAL_SBE; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 124 AA; 13515 MW; B7038CF79A83742B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        5; IPR001047; Ribosomal_S8E.
F01201; Ribosomal_S8e; 1.
PD005658; Ribosomal_S8E; 1.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE005076; AAG19920.1; -
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Pfam; PF01201
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Search completed: May 12, 2003, 15:36:39 Job time : 3.32 secs

1 RGDA 4 ||||| 47 RGDA 50

9 9 Q29783 homo sapien Q9pau0 xylella fas Q9dk41 human immun Q9fzt5 pseudomonas Q9nm57 leishmanla

Q8s2d8 oryza sativ Q8z7w3 salmonella Q8z7w3 salmonella Q9pds1 xylella fas Q98fe9 rhizobium 1

Q8w3b8 oryza sativ. Q9pd18 xylella fas Q8zv78 pyrobaculum Q95y01 caenorhabdi Q29783 homo saplen

Q9PD18 Q8ZV78 Q95Y01 Q29783

Q9PAU0 Q9DK41

Q8x8q7 escherichia Q8tk40 methanosarc

OSKE84 Dacillus ha OSKE84 Dacillus ha OSHE8 pseudomonas OSE39 molluscum c OSE37 mycobacteri OSE37 mycobacteri OSE073 mycobacteri OSE073 mycobacteri

09HTA8 Q8RM68 Q98239

Q827W3 Q9PDS1 Q98FE9 Q9KE84

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us-09-909-348-3.rspt

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A Simpson A.J.G., Rethach F.C., Arruda P., Abreu F.A., Acencio M., RA Darrenga R., Alves L.M.C., Arruda P., Bala G.S., Baptista C.S., RA Barros M.H.; Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Buenco M.H.; Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Buenco M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., RA Coutinho L.L., Cristofani M., Dias Neto E., Docena C., El-Dorry H., Fardicani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro G., El-Dorry H., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Fullan L.R., RA Fredincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro G. M., Ranco M.C., Lopes S.L., Kitajima J.P., RA Garnier M., Goldman E.E., Laighet E.L., Kitajima J.P., RA Krieger J.E., Kuranae E.E., Laighet F., Lambais M.R., Leicos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Mardeira A.M.B.N., Madeira H.M.F., Matukuma A.Y., RA Menck C.F.M., Martins E.A.L., Martins E.M.F., Matukuma A.Y., RA Menck C.F.M., Mincca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagail M.A., Nascimento A.L.T.O., Netto L.E.S., Anderlara M.C., de Oliveira R.C., Palmieri D.A., Paris A., Ra Pelvoto B.R., Poereira B.R., Oliveira M.A., Redensa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., R. de Silva A.C.R., da Silva A.M., dr. Jr., R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf0386.
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MEDLINE-20365717; PubMed-10910347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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8888
 Xylella
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Q9PGB6
Ogogbe xylella fas Ogyadv3 erythrobact Ograds eremoanaer Ogruzl zee mays (m Ogno4) macaca fasc Ogruds zee mays (m O6773 mycobacteri Oggs83 chimpanzee Ogls77 raistohium 1 Ogsyg0 raistohium 209773 leishmania Oguyk6 agrobacteri Ogwyvo Witte spot Ogwyvo Witte spot Ogwyvo Mitte spot Ogwyvo maistonia s Ogy128 raistonia s
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                                                                          May 12, 2003, 15:32:37; Search time 9.04 Seconds (without alignments) 91.171 Million cell updates/sec
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         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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Q9NO41
Q8RUD5
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098LS7
098LS7
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08VJV6
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Gapop 10.0 , Gapext 0.5
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p_invertebrate:*
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Maximum DB seq length: 200000000
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21
1 RGDA 4
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ALIGNMENTS

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"A complete sequence of T. ter
Genome Res. 12:689-700(2002).
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nes 4; Conserv
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Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID-119072;
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *Nucleotide sequences of genes coding for photosynthetic reaction centers and light-harvesting proteins of Erythrobacter litoralis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J. Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling Tan H., Chen R., Wang J., Yu J., Yang H.;
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythrobacter sp. MBIC3960.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                           h 100.0%; Score 21; DB 16; Length 45; Similarity 100.0%; Pred. No. 2.9e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 2; Length 48; Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related aerobic photosynthetic bacteria.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO27515; BAA78669.1;
Interpro; IPRO1552; Acyl-CoA_dh.
PROSITE; PSO0073; ACYL_COA_DH.2; UNKNOWN.1.
SEQUENCE 48 AA; 4980 MW; D663EAD05EA8079B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein TTE2436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12; Created)
01-NOV-1999 (TrEMBLrel. 12; Last sequence update)
01-DEC-2001 (TrEMBLrel. 19; Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 AA
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STRAIN-MB4T / JCM11007;
MEDLINE-21992816; PubMed-11997336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoanaerobacter tengcongensis.
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Similarity 100.0%;
4; Conservative 0
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erythrobacter.
NCBI_TaxID=94771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              centers and 1
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27 RGDA 30
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Q8R7H3
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Q9XDV3
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[1]
SEQUENCE FROM N.A.
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=VARIOUS STRAINS;
Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
Morgante M., Rafalski J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frequency, haplotype structure and linkage disequilibrium in a maize inbred lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Unnamed protein product.
Unamed protein product.

Budacae fassicularis (Crab eating macaque) (Cynomolgus monkey).
Eukarybta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                      54;
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                                                                                                                                                                                                           Indels
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                                                                                                                                                         Length
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                                         EMBL, AE013185, AAM25571.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 54 AA; 6252 MW; 0A9C818C07DD905B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Acetyl-CoA C-acyltransferase-like protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 AA; 5959 MW; 5C09DAC7224451D0 CRC64;
tengcongensis genome.";
                                                                                                                                                   100.0%; Score 21; DB 16; 100.0%; Pred. No. 3.5e+02;
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                           Mismatches
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NON_TER 1 1
SEQUENCE 55 AA; 5959 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel, 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF498485; AAM14501.1
EMBL; AF498486; AAM14502.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF498463; AAM14479.1
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. IVANA, CV. D71-4HT, AND CV. H60;
Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
Morgante M., Rafalski J.A.;
"SNP frequency, haplotype structure and linkage disequilibrium in
elite maize inbred lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Corynebacterineae; Mycobacteridae; Nycobacterium NCBL_TaxID-1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Garnier T., Churcher C., Harris
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                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF498474; AAM14490.1; -.
EMBL; AF498476; AAM14492.1; -.
EMBL; AF498479; AAM14492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 21, Last annotation update)
Acetyl-CoA C-acyltransferase-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 AA; 6185 MW; DC4596C76E4451A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Complete proteome.
7 AA; 5849 MW; 62858455BD7D0F2E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 10;
100.0%; Pred. No. 3.7e+02;
iive 0; Mismatches 0;
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100.0%; Score 21; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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01-JUL-1997 (TrEMBLRel. 04, La
01-MAR-2002 (TrEMBLRel. 20, La
Hypothetical protein Rv0666.
RV0666 OR MTC1376.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acyltransferase; Transferase.
NON_TER 1 1
SEQUENCE 57 AA; 6185 MW; I
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Tuberculist; Rv0666; -.
Hypothetical protein; Comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                       NCBI_TaxID-4577;
                                                                                                                   Zea mays (Maize)
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33 RGDA 36
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006773
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
                                                                                                                                                                                 Gaps
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Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
Morgante M., Rafalski J.A.;
Morgante W., Rafalski J.A.;
"SNP frequency, haplotype structure and linkage disequilibrium in
elite maize inbred lines.";
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"Isolation of full-length cDNA clones from macaque brain cDNA libraries.";
Submittes.";
Submittes.000) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO46091; BAB01673.1; -.
SEQUENCE 57 AA; 6250 MW; 300DE0464A4897A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 21; DB 10; Length 57; larity 100.0%; Pred. No. 3.7e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                       Length 57;
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                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TIEMBLIEL. 21, Created)
01-JUN-2002 (TIEMBLIEL. 21, Last sequence update)
01-JUN-2003 (TIEMBLIEL. 21, Last annotation update)
Acetyl-CoA C-acyltransferase-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 AA; 6203 MW; DC4596C27A4451A8 CRC64;
                                                                                                                                100.0%; Score 21; DB 6; I 100.0%; Pred. No. 3.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                          4; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE
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                                                                                                                                                                        Matches
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Q8RUD4
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RESULT 9 Q8QS83

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LM28.210.
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_raxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL390935; CAC00934.1; -
                                                                                                                                                                        Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 16; Length 64; 100.0%; Pred. No. 4.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Complete proteome.
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                                                  (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) Probable hypothetical 32.4 kba protein (Fragment).
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OBUJK6;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
       64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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01-0CT-2000 (TEMBLE). 15, Last seq
01-0CT-2000 (TEMBLE). 15, Last ann
       PRT;
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                                                                                                                        Hypothetical protein RSc1708
RSC1708 OR RS02894.
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       PRELIMINARY;
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Best Local Similarity
4; Conserve
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                                                  01-MAR-2002 (
01-MAR-2002 (
01-MAR-2002 (
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RGDA 31
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SEQUENCE
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Q9N7K3;
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Q8UJK6
ID Q8UJK
AC Q8UJK
DT 01-JU
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"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                      Davison A.J., Akter P., Dolan A., Wright K.M., Addison C., Alcendor D.J., Hayward G.S., McGeoch D.J.;
"The human cytomegalovirus genome revisited.";
Submitted (FEB-2002) to the EWBL/GenBank/DDBJ databases.
EWBL; AF480884; AAM00654.1; -
SEQUENCE 58 AA; 6789 MW; 27400659BBDZBAD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 16; Length 5
100.0%; Pred. No. 3.8e+02;
ive 0; Mismatches 0; Indels
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EMBL; AP002996; BAB48386.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 59 AA; 6059 MW; 4EE77EF3940E6633 CRC64;
                                                                                                                                                                                                                                                                 chimpanzee cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaharpesvirinae; Cytomegalovirus.
                                                                                                                                                                 -JUN-2002 (TrEMBLrel. 21, Created)
-JUN-2002 (TrEMBLrel. 21, Last sequence update)
-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ms10897.
                                                                                                                        58 AA
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nes 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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2 RGDA 5
24 RGDA 27
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RESULT 10 Q98LS7

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RESULT 11 Q8XYQ0

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Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H., Lo C.F., Kou G.H.;
Indertification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells."; Virology 293:44-53(2002).
                                                                            Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J., Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
"Identification and characterization of a shrimp white spot syndrome virus (WSV) gene that encodes a novel chimeric polypeptide of cellular type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lo C.-F., Kou G.-H.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332093; AAL33282.1; -.
EMBL; AF446570; AAL89202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AA; 7417 MW; 6C31737FF210FB62 CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RSc3433.
RSC3433 OR RS01813.
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100.0%; Pred. No. 4.5e+02;
1ve 0; Mismatches 0;
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100.0%; Pred. No. 4.5e+02;
tive 0; Mismatches 0;
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                                                       MEDLINE-20517548; PubMed-11062040;
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             STRAIN-TAIWAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-TAIWAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 RGDA 33
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Q8XTW3
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";
                                                                                                                                                                                              MEDLINE-21608550; PubMed-11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McCleilland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurcollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houniel K., Gordon J., Yaudin M., Tartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sar C., Strub G., Clen C., Slater S.; Genome sequence of the plant pathogen and blotechnology agent Agrobacterium tumefaciens 558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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MEDLINE-21548311; PubMed-11689662;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 16; Length 68; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l protein; Plasmid; Complete proteome.
68 AA; 8005 MW; 5CABE406D75F93A8 CRC64;
                                                                   Agrobacterium Tumefaciens (strain C58 / ATCC 33970)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical protein Atu5470. ATU5470 OR AGR_PAT_693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White spot syndrome virus (WSSV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virol. 75:11811-11820(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE008968; AAL46157.1; -.
EMBL; AE007916; AAK90845.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 294:2323-2328(2001)
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Les 4; Conservative
                                                                                                                                      Rhizobiaceae; Rhizobium.
NCBI_TaxID-176299;
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RGDA 39
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SEQUENCE 68
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Best Loca Matches

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RESULT 14 Q8VAV0

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virus.

Search completed: May 12, 2003, 15:38:43 Job time: 12:04 secs

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Scoring table:

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Platelet membrane
Thrombin peptide d
Bovine zeta 2 pret
Bovine prethrombin
Bovine prothrombin
Thrombin B chain a
Modified RGD pepti
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Human CD4-thrombin
Prothrombin (PT).
Human prothrombin
Human prothrombin
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Mutant thrombin R2
Mutant thrombin W5
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Amino acid sequenc
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Human preprothromb
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                                            Mutant
                                 Mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell growth; adhesion; promotion; medical treatment; injury; biotissue; bone reinforcement; nerve regeneration; HMP resin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Material for medical treatment comprises new peptide - used covering injuries, promoting adhesion of bio-tissues, bone reinforcing and nerve regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell growth/adhesion promoting peptide #1
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                                                                                                                                                                                                                                                                   AAR35763
AAW11546
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW10750
AAB83282
                                           AAR74780
AAR76033
AAR76034
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                                                                                                                                                                   AR<sub>7</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 12; 14pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KURS ) KURARAY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-076400/07.
JP10316581-A.
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   AAW83414;
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   Human zeta 2 preth
Human thrombin Asn
Wild-type thrombin
Mutant thrombin K5
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Human thrombin pep
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46.591 Million cell updates/sec
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| SIDS2/gcgdata/geneseq_geneseqp_embl/AA1980.DAT:*
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               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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141
1 AGTRYKPDEGKRGDACEGDSGGPFV 25
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Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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AAE22563
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a new nerve regenerative material which contains a peptide immobilised to a base which consists of a polysaccharide gel such as alginic acid. Sequences AAB12886-B12899 represent examples of the peptides used in the nerve regeneration material. The peptide containing material causes nerve cell proliferation and also causes axonal extension. The material can be used for the treatment of central or peripheral nervous system disorders,
The present invention describes a material for medical treatment which comprises one or more peptides of the formula XADEGJIMProQY, or their salts, immobilised on a substrate: where X = H, CH3CO or CH3COLys;
A = Ser or Thr; D = ILe Val or Leu; E = Lys or Arg; G = ILe, Val or Leu; J = Gly or Ala; Q = Gly, Val or Leu; M = Gly or Ala; Q = Gly, Ala or Gly-Lys-Lys-Gly; Y = OH or NH2. Also described is an agent for cell growth promotion and/or cell adhesion promotion containing the above peptide or its salt as the active component. The peptide and its salt can be used for covering injuries, promoting adhesion of biotissues, bone reinforcing and nerve regeneration. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nerve regeneration; nerve cell proliferation; axon extension; treatment;
                                                                                                                                                                                                                                                                  Gaps
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disorder; head injury; cerebrovascular disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23;
                                                                                                                                                                                                                                 Length 23;
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                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                specifically claimed peptide of the present invention
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1larity 100.0%; Pred. No. 1.6e-07;
Conservative 0; Mismatches 0;
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Pred. No. 1.6e-07;
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                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                 85.8%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nerve regeneration material
                                                                                                                                                                                                                                                                                                                                                                                                          AAB12893 standard; peptide; 23
                                                                                                                                                                                                                                                                                                             3 YKPDEGKRGDACEGDSGGPFV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TANI/) TANIHARA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-415772/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AA;
                                                                                                                                                                                                23 AA;
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Best Local Simi
Matches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB12893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spinal
                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New synthetic neutrophil cell chemotactic peptides, useful for generating antibodies for modulating neutrophil chemotaxis in immune response and wound healing -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                          Neutrophil cell chemotactic; wound healing; inflammation; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; proteolytically activated receptor for thrombin; neutrophil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a synthetic peptide (I) which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                       Human thrombin receptor binding domain peptide SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 121; DB 22;
Pred. No. 1.6e-07;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHRY-) CHRYSALIS BIOTECHNOLOGY INC.
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                                                                                                                                                   AAB70363 standard; peptide; 23 AA
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100.08; Fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YKPDEGKRGDACEGDSGGPFV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0330594
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                                                                                                                                                                                                                                                 02-MAY-2001 (first entry)
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Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-202003/20
                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6184342-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1994;
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Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteolytically activated thrombin receptor
                                                                                                                                                                                                                                                                           The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (NPAR). The method is used in human or veterinary medicine for the treatment of arthritic
                                                                                                                                                                                                                                                                                                                                                           joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide derivative which serves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Promoting cardiac tissue repair, stimulating revascularisation, stimulating vascular endothelial cell proliferation, and inhibiting vascular occlusion by using angiogenic thrombin derivative peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombin; revascularisation; vascular occlusion; tissue repair; vulnerary; vasotropic; cardiant; anglogenesis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombin-derived peptide used to promote cardiac tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12..23
/note= "serine esterase conserved sequence"
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                                                                       Stiernberg J, Bergmann J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.8%; Score 121; DB 23;
100.0%; Pred. No. 1.6e-07;
11ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.0%,
100.0%; Pre-
                                                                                                                                                                                                                                       Claim 12; Page 25; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2001; 2001WO-US21944
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                            (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.8
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TEXA ) UNIV TEXAS SYSTEM
                                                                       Carney DH, Crowther RS,
                                                                                                            WPI; 2002-268953/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-179665/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  a NPAR agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary; vasc
therapy; human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200204008-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carney DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM50858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
AAM50858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel synthetic peptides and antibodies which are potent chemotactic agents for neutrophils. The peptides of the invention minic the activity and role of the cleavage fragment of the proteolytically activated receptor for thrombin (PART). They are useful for stimulating or modulating neutrophil cell chemotactic migration or are useful for modulating neutrophil recultment to a wound site for an antibody. In particular, the peptides of the invention are useful for modulating neutrophil recultment to a wound site for enhancing or inhibiting inflammation and early effects in wound healing. They are also useful for modulated neutrophil chemotaxis in immune tesponse. The present sequence is high affinity receptor binding domain of human thrombin. This peptide is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage repair; arthritic joint; traumatic injury;
ly activated thrombin receptor; NPAR; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                            New synthetic peptide neutrophil cell chemotactic agents, useful for stimulating or modulating neutrophil cell chemotactic migration, particularly for modulating neutrophil recruitment during immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
chemotactic agent; PART; inflammation; wound healing; chemotaxis; immune response; vulnerary; thrombin; receptor binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.8%; Score 121; DB 23;
100.0%; Pred. No. 1.6e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy; implantation; thrombin peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human thrombin peptide derivative #2
                                                                                                                                                                                                                                                                       (CHRY-) CHRYSALIS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE20159 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 3; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             response or in wound healing
                                                                                                                                                                                     05-FEB-2001; 2001US-0777328
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                                                                                                                                                                                                                                                                                                                Ramakrishnan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-2002 (first entry)
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-371207/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cartilage growth; canon-proteolytically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 AA;
                                                                                                   JS2002032314-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200207748-A2.
                                                                                                                                                                                                                              28-OCT-1994;
                                                              Homo sapiens
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                                                                                                                                              14-MAR-2002
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RESULT 5 AAE20159

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                                                                                                                                                                                                                                                                                                                                                     Gaps
                                              The present peptide comprises a thrombin-derived peptide, TP508, that includes a thrombin receptor binding domain sequence (see also AAM50856) and a serine esterase conserved sequence (see also eardiectissue repetide is used in a claimed method for promoting cardiac tissue repair. It is administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. The thrombin derivative peptide is also used in claimed methods of stimulating revascularisation, stimulating vascular endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exosite assay for agents that inhibit catalytic cleavage of prothrombin - at sites away from the active site of prothrombinase, also new inhibitors, potentially useful as anticoagulants
                                                                                                                                                                                                   proliferation, inhibiting vascular occlusion, and inhibiting restenosis following balloon angioplasty, in which case it may be coated onto the catheter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prothrombin; exosite assay; anticoagulant; blood clot; thrombin; cardiovascular disease; stroke; haematological disorder.
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                                                                                                                                                                                                                                                                                                                  Length 23;
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                                                                                                                                                                                                                                                                                                              85.8%; Score 121; DB 23;
100.0%; Pred. No. 1.6e-07;
1ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99115 standard; protein; 116 AA
            Claim 4; Page 19; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                      25
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97US-0048864
                                                                                                                                                                                                                                                                                                                                                                                      5 YKPDEGKRGDACEGDSGGPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human zeta 2 prethrombin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                               23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krishnaswamy S;
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                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                Query Match
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reaction mixture, quenching them; and (d) assaying for concentration of Th. Alternatively, in the initial solution S is replaced by the same concentration of Xa (less than the amount of Va), and reaction is started by adding S. Also described in the present invention are inhibitors (A') had having 1650 less than 1 mu M identified by this assay. (A') are potentially useful as a new class of anticoagulants for treatment of cardiovascular disease, stroke and haematological disorders. The method substrate specificity in catalytic formation of Th. The present sequence represents human zeta 2 prethrombin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prothrombin mutants having one or more changes in amino acid sequence compared with the natural protein and having 0-10% (preferably 0-0.25% of the activity of the natural protein are claimed, provided that the changes in amino acid sequence do not affect the capacity of the mutants to bind to specific ligands and receptors. The mutants have greatly reduced clotting activity and are useful as antagonists of thrombin inhibitors such as hirudin, hepsin and anti-thrombin III. The mutations may also result in changes to the in vivo half-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prothrombin; mutant; mutein; platelet aggregation; blood clotting; coagulation; reduce; decrease; hirudin; heparin; anti-thrombin III; antagonist; D99N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Wild-type Asp residue has been replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prothrombin mutants with reduced clotting activity - useful as antagonists of thrombin inhibitors or for anticoagulant therapy
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                     85.8%; Score 121; DB 20;
illarity 100.0%; Pred. No. 6.9e-07;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- thrombin_Asn99
Misc-difference 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human thrombin Asn99 mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-065455/06
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMO ) IMMUNO AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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prothrombin. The half-life may be reduced to less than 10 minutes the mutant prothrombin may have an extended half-life of more than
                                                                                                                                                                                                                              Gaps
                     1 hour, making it useful as an anticoagulant and to inhibit side-
effects of anti-coagulant treatment. They are converted to inactive
thrombin and are able to compete with native, active thrombin for
blinding to receptors. The present sequence represents the thrombin
mutant which is derived by trypsin cleavage of a specifically
claimed human prothrombin mutant in which Asp at position 419 is
changed to Asn. The thrombin Asn99 mutant was found to have only
0.24% of the activity of wild-type thrombin on a chromogenic
                                                                                                                               (Note: This sequence does not appear in the specification and has been produced by modifying the wild-type sequence of human prothrombin which appears in figure 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombin derivs with segregated pro- and anticoagulant activities useful for treating thrombotic disorders but also diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence reresents wild-type (reference) thrombin. Mutants of this sequence (AAR7476-80 and AAR76033-41) have at least 80% monology with thrombin, and are capable of protein-c activation without significant fibrinogen clotting activity, and vice versa (specifically have a ratio of protein-c activity to fibrinogen clotting activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombin; oligonucleotide-directed mutagenesis; procoagulant;
                                                                                                                                                                                                     85.8%; Score 121; DB 18; Length 259; 100.0%; Pred. No. 1.4e-06; 1.4e-0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                anticoagulant; protein engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 37..295
                                                                                                                                                                                                                                                                                                                                      AAR74775 standard; Protein; 295 AA.
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                                                                                                                                                                                                                  Best Local Similarity 100.0%; Pr
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                  190 YRPDEGKRGDACEGDSGGPFV 210
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93US-0152657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of tumours, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibbs CS, Leung LLK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-194103/25.
                                                                                                                                                                                                                                                                                                                                                                                                           Wild-type thrombin.
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12-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                              AAR74775;
                                                                                                                                                                                Sequence
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thrombin). The mutant thrombin sequences, produced in recombinant cell culture or by in vitro methods, and are used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombin; oligonucleotide-directed mutagenesis; procoagulant;
                                                                                                                                                                 Length 295;
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                                                                                                                                                              Score 121; DB 16;
Pred. No. 1.6e-06;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Lys in wild-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticoagulant; protein engineering; ss
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                                                                                                                                             85.8%; Sc._
100.0%; Pre
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93US-0152657
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                                                                                                                                                                                                             21; Conservative
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                                                                                                                                                              Ouery Match
Best Local Similarity
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                                                                                                                  295 AA;
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12-NOV-1993;
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AAR74777

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Protein

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The mutant thrombin sequence, generated by oligonucleotide-directed mutagenesis, has at least 80% homology with thrombin, and is capable of protein-C activation without significant fibrinogen clotting activity, and vice versa (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin). The mutant thrombin is produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rnrombin derivs with segregated pro- and anticoagulant activities
useful for treating thrombotic disorders but also diagnosis,
treatment of tumours, etc.
                                                                                                                                                                       mutagenesis; procoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 121; DB 16;
Pred. No. 1.6e-06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                               /note= "Glu in wild-type" 37..295
                                                                                                                                                                                                                                                                                                                                      37..295
/note= "mature protein"
                                                                                                                                                                     Thrombin; oligonucleotide-directed muta
anticoagulant; protein engineering; ss
                                                                                                                                                                                                                                                                         Location/Qualifiers
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  AAR74778 standard; Protein; 295 AA.
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100.0%; Pre
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les 21; Conservative
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                                                                                                                              Mutant thrombin E229F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leung LLK,
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12-NOV-1993;
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AC AAR7
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llarity 100.0%; Pred. No. 1.6e-06;
Conservative 0; Mismatches 0;
Pred. No. 1.6e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Glu in wild-type" 37..295
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Best Local Similarity 100.0%; F
Matches 21; Conservative 0;
                                                                                    226 YKPDEGKRGDACEGDSGGPFV 246
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93US-0152657
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Best Local Similarity
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12-NOV-1993;
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Gaps

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Sequence

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RESULT 12 AAR74778

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Length 295; Indels Thrombin; oligonucleotide-directed mutagenesis; procoagulant; anticoagulant; protein engineering; ss.

Protein

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The mutant thrombin sequence, generated by oligonucleotide-directed mutagenesis, has at least 80% homology with thrombin, and is capable of protein-C activation without significant fibrinogen clotting activity, and vice versa (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin). The mutant thrombin is produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
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100.0%; Pred. No. 1.6e-06;
11ve 0; Mismatches 0;
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/note= "mature protein"
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100.0%; Pre
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                                     94WO-US13104
                                                                       94US-0258038.
93US-0152657.
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Matches 21; Conservative
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                                                                                                                           (GILE-) GILEAD SCI.
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                                     14-NOV-1994;
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12-NOV-1993;
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   18-MAY-1995
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                                                   /note= "Glu in wild-type"
37..295
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/note= "mature protein"
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/note= "mature protein"
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93US-0152657
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                                                 Misc-difference
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12-NOV-1993;
Homo sapiens
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AAR74780;

RESULT 14 AAR74780

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Protein

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Gaps

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Length 295; Indels

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Gibbs CS, Leung LLK, Tsiang M;

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WPI; 1995-194103/25.

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Thrombin derivs with segregated pro- and anticoagulant activities ruseful for treating thrombotic disorders but also diagnosis, provided for thrombotic segment for mutant thrombotic segment for mutagenesis, has at least 80% homology with thromboth, and is capable of protein-C activation without significant fibrinogen conting activity, and vice versa (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin). The mutant thrombin of a produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.

SQ Sequence 295 AA;
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Query Match 85.8%; Score 121; DB 16; Length 295; Best Local Similarity 100.0%; Pred. No. 1.6e-06; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps Oy 5 YKPDEGKRGDACEGDSGGPFV 25

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Search completed: May 12, 2003, 15:36:06 Job time : 72.5 secs

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Gaps
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Patent No. 6146824
GENERAL INFORMATION:
APPLICANT: BAR-SHAVIT, RACHEL
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TUTHER OF INVENTION: PHARMACEUTICAL COMPOSITIONS
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: "PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 5.3e-11;
Mismatches 0:
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                                        US-08-955-471-1
US-09-667-570A-3
PCT-US92-10242-1
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,088
FILING DATE: 27-JAN-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: OLIFF, JAMES A
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 40455
TELEFROMUNICATION INFORMATION:
TELEFROM
                                                                                                                                                          5270178-16
                                                                                                                                            5270178-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
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100.08; PIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 21; Conservative
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Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 4, Appli
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Sequence 11, Appli
Sequence 11, Appli
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                                                                                              May 12, 2003, 15:33:37; Search time 24 Seconds (without alignments) 30.649 Million cell updates/sec
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Sequence 51,
Sequence 51,
Patent No. 52
Patent No. 52
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Sequence 2,
Sequence 2,
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Patent No.
Patent No.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-344-483-52

US-08-358-269-10

US-09-410-882-10

US-08-255-411-4

US-08-955-411-4

US-08-955-411-4

US-09-117-708-14

US-09-117-708-14

US-09-117-708-14

US-08-951-11357-3

US-08-951-11357-3

US-08-951-11357-3

US-08-981-088-3

US-08-944-483-51

US-08-941-088-4

US-08-941-088-4
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US-09-065-872-2
US-09-667-570A-2
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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141
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Perfect score:
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Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL POLYPEPTIDES AND COAGULATION TITLE OF INVENTION: THERAPY NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,368
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                            7.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 121; DB 3;
Pred. No. 8.2e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                       85.8%; Score 121; DB 4;
100.0%; Pred. No. 7.2e-10
:Ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/258,038
FILING DATE: 10-UUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: GILEAD SCIENCES, INC
353 LAKESIDE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.8%; Sc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08338368
Patent No. 6110721
GENERAL INFORMATION:
APPLICANT: GIBBS, CRAIG S.
APPLICANT: TSIANG, MANUEL
APPLICANT: TSIANG, MANUEL
                                                                                                                                                                                                                                                                                                                                           190 YKPDEGKRGDACEGDSGGPFV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 YKPDEGKRGDACEGDSGGPFV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FELECOMMUNICATION INFORMATION: TELEPHONE: 415-574-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                        5 YKPDEGKRGDACEGDSGGPFV 25
                                 INFORMATION FOR SEQ ID NO: 52: SEQUENCE CHARACTERISTICS: LENGTH: 259 amino acida TYPE: amino acid
                                                                                                                                                           TOPOLOGY: 'linear'; MOLECULE TYPE: No. 6232456e
US-08-944-483-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: HENSLEY, MAX D. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-338-368-2
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 21; Conserva
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CALIFORNIA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                         GENERAL INFORMATION:
APPLICANT: CAREY, DARRELL H.
APPLICANT: RAMAKRISHNAN, SHYAM
APPLICANT: RAMAKRISHNAN, SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHAP: 00.2
CURRENT APPLICATION NUMBER: US/08/330,594C
CURRENT FILING DATE: 1994-10-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-08-330-594-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 23
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85.8%; Score 121; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 21; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BECKET, Cheryl L. REGISTRATION NUMBER: 35,441 REFERENCE/DOCKET NUMBER: 6183.US.01
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NOVEL SERINE PRO'
AND METHODS USER'
OF THE PROSTATE
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                                                     Sequence 8, Application US/08330594C Patent No. 6184342
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STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELECOMMUNICATION INFORMATION:
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ZIP: 60064-3500
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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APPLICATION NUMBER: US
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TITLE OF INVENTION: NOVI
TITLE OF INVENTION: AND
TITLE OF INVENTION: OF I
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-944-483-52
                                       US-08-330-594-8
                                                                                                                                                                                                                                                                             SEQ ID NO 8
LENGTH: 23
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STATE:
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Protease-Derived Polypeptides and eptide Antibodies, Systems and Therapeutic Methods
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STREET: 10666 No. 5679639th Torrey Pines Road, TPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOCTURED STATES SOCTURED BY SOCTURED BY SOCTURED BY SOCTURED BATA:
CURRENT APPLICATION DATA:
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 121; DB 4;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Peptide Antibodies, Sifor Inhibiting Coagulation 10
                                  FILING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/558,269
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CRI-001CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SED ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
FILING DATE: MATCHERISTICS:
LENGTH: 376 amino acids
                    US/09/410,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: GTIffin, John H.
TITLE OF INVENTION: Serine Proteas
TITLE OF INVENTION: Anti-Peptide P
TITLE OF INVENTION: for Inhibiting
NUMBER OF SEQUENCES: 10
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS
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Best Local Similarity 100.
Matches 21; Conservative
CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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; MOLECULE TYPE: protein
US-09-410-882-10
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US-09410-882-10
Sequence 10, Application US/09410882
Fatent No. 6287561
GENERAL INFORMATION:
APPLICANT: PATHOGEN-TARGETED BIOCATALYSTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                         Sequence 10, Application US/08558269
Patent No. 5961973
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,269
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: VIncent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CRI-001CP2
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                      CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.8%; Sc
Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-7400
TELEFRA: (617) 227-5401
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 YKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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COUNTRY: USA
02109
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                                                                                                                                                                                                                                                                                                 Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: RADITSHC, Martin; FRIEDRICH, Thomas;
APPLICANT: BOLLSCHWEILER, Claus; SCHMIDT, Martin;
APPLICANT: HOEFFERN, Mans Wolfgang; SCHWEDEN, Juergen;
APPLICANT: and RUBESAMEN, Klaus
TITLE OF INVENTION: Thrombin muteins as antidote for
TITLE OF INVENTION: thrombin inhibitors
                           NAME/KET: Region
LOCATION: 1..320
OTHER INFORMATION: /note= "Prothrombin Light Chain"
                                                                                                                                                                                                        /note= "Prothrombin Heavy Chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM AT-compatible, Pentium processor OPERAITMS SYSTEM; Whidows 95
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,708
FILING DATE: O4-ANG-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                              Score 121; DB 2;
Pred. No. 1.7e-09;
0; Mismatches 0;
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Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09117708 Patent No. 6060300 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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Best Local Similarity 100.0%; P

Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & We
                                                                                                                                                                            ; LOCATION: 321..579
; OTHER INFORMATION:
US-08-955-471-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20036
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US92-10242-4
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                                                                                                                     FEATURE:
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Rolf M.
Sorine Protease-Derived Polypeptides and
Sorine Protease. Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                               LOCATION: 1.320
OTHER INFORMATION: /note- "Prothrombin Light Chain"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Office of Patent Counsel, The Scripps
E: Research Institute
10666 No. 5968751th Torrey Pines Road, TPC
                                                                                                                                                                                                                                                                                                                                                                                                             /note- "Prothrombin Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULTRARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.8%; Score 121; DB 1;
100.0%; Pred. No. 1.7e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSRI263.0C1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
ATTORNEY, FAGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFRONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08955471 Patent No. 5968751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 YKPDEGKRGDACEGDSGGPFV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YKPDEGKRGDACEGDSGGPFV 25
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amino acid

    579 amino acids
amino acid

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Best Local Similarity 100.
Matches 21; Conservative
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SEQUENCE CHARACTERISTICS
                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: GLIffin, JG
APPLICANT: Mesters, RG
TITLE OF INVENTION: SG
TITLE OF INVENTION: AT
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      HAME/KEY: Region LOCATION: 321..579 CTHER INFORMATION: US-08-295-411-4
                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      La Jolla
                                                                                                                                          HYPOTHETICAL: N
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-955-471-4
                        LENGTH:
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Gaps

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Length 615;
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APPLICANT: Holly, Richard D.
APPLICANT: FOSIEr, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Townsend and Townsend
STREET: Twentieth Floor
CITY: San Francisco
                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 1;
Pred. No. 1.8e-09;
0; Mismatches 0;
                                                                                                                                                                                               FILING DATE: 19921230
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MRR-1992
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PAIMELES, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
                                                                                                                                                                                    APPLICATION NUMBER: US/07/998,972A
FILING DATE: 19921230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.08; Pr
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                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 amino acids
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-998-972A-3
             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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    Serine Protease-Derived Polypeptides and
Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-998-972A-3

Sequence 3, Application US/07998972A

Fatent No. 54/6777

FENERAL INFORMATION:

APPLICANT: Holly, Richard D.

APPLICANT: Foster, Donald C.

TILE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSES: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,

STREET: Twentieth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 321..579
; OTHER INFORMATION: /note= "Prothrombin Heavy Chain"
PCT-US92-10242-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "Prothrombin Light Chain
                                                                                                          ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILIGATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 YRPDEGKRGDACEGDSGGPFV 530
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SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Seri
TITLE OF INVENTION: Anti
TITLE OF INVENTION: for
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Twentieth F
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Region
LOCATION: 1.320
OTHER INFORMATION:
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FEATURE:
                                                                                                                                                                                                                      COUNTRY:
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Query Match
Best Local Similarity
Matches 21; Conserva
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OPERATING SYSTEM:
    Query Match
Best Local Similarity
Matches 21; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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PCT-US92-11357-3
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                                                                                                                                                                                                                                                                                                                       Length 615;
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MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,261
FILING DATE: 05-JUN-1995
CLASSIFICATION: A24
PRICA STFICATION AAA:
APPLICATION NUMBER: US 07/998,972
FILING DATE: 31-DEC-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-DEC-1992
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATENTED NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TRELECOMMUNICATION INFORMATION:
TRELECOMMUNICATION INFORMATION:
TRELECOMMUNICATION INFORMATION:
TRELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...ukussee: ...uukess:
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentleth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                       Score 121; DB 1; 1
Pred. No. 1.8e-09;
0; Mismatches 0;
                                 RECISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 1395;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9603
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 anino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    Query Match 85.8%; Soc
Best Local Similarity 100.0%; Pi
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               546 YKPDEGKRGDACEGDSGGPFV 566
                                                                                                                                                                                                                                                                                                                                                                                                         5 YKPDEGKRGDACEGDSGGPFV 25
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ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven
                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-463-953-3
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    Length 615;
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                                                                                                                                                                                                                                                                    APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: FOSter, Donald C.
TILE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Townset Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US92/11357
FILING DATE: 19921230
    Score 121; DB 1; Pred. No. 1.8e-09;
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9211357
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fischer, Bernhard
Schlokat, Uwe
Mitterer, Artur
Falkner, Falko-Guenter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 8, Application US/08952967
; Patent No. 6086871
85.8%; Scilarity 100.0%; P. Conservative 0;
                                                                                                           546 YKPDEGKRGDACEGDSGGPFV 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
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                                                                                     5 YKPDEGKRGDACEGDSGGPFV 25
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
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PCT-US92-11357-3
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APPLICANT:
APPLICANT:
APPLICANT:
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CITY: Washington
CITY: Washington
COUNTR: U.C.
COUNTR: U.C.
COMPUTE: D.C.
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC compatible
APPLICATION NUMBER: US/08/952,967
FILING DATE: 12-JUN-1996
RILNG DATE: 12-JUN-1996
RILNG DATE: 12-JUN-1996
RILNG DATE: 13-JUN-1995
ATPLICATION NUMBER: AT A 1006/95
FILING DATE: 13-JUN-1995
ATPLICATION NUMBER: AT A 1006/95
FILING DATE: 13-JUN-1995
APPLICANT: E1bl, Johann
TITLE OF INVENTION: PROTHROMBIN DERIVATIVES
NUMBER OF SEQUENCES: 22
ANDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
SITY: Mashington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,715
REFERENCE/FOUNDER: 065691/0127
TELECOMONICATION INFORMATION:
TELEFONE: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
TELER: 904.36
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
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; MOLECULE TYPE: protein
US-08-952-967-8
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Search completed: May 12, 2003, 15:40:40 Job time: 24 secs

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Ouery Match
85.8%; Score 121; DB 3; Length 622;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 21; Conservative 0; Mismatches 0; Indels

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Searched:

Database

Result

Sequence:

Run on:

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Sequence 7
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Bublication No. US20020182205A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Crowther, Roger S.
APPLICANT: Simons, David J.
APPLICANT: Stand, Milliam R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
FILE REFERENCE: 3033.1002-004
CURRENT FILING DATE: 2002-01.16
PRIOR PRILING DATE: 2001-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
SEQ ID NOS: 6
SOFTWARE: FEASTSED for Windows Version 4.0
SEQ ID NO 5
LENOTH: 25
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Best Local Similarity 100.0%; Pred. No. 8.5e-13;
Matches 25; Conservative 0; Mismatches 0;
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OTHER INFORMATION: fragment of human prothrombin
05-10-050-692-5
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US-09-909-348-5
Sequence 5, Application US/09909348
; Patent No. US20020042373A1
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ORGANISM: Artificial Sequence
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Sequence 4, Appli
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Sequence 6, Appli
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                                                                                                                                                                                           May 12, 2003, 15:38:52 ; Search time 48.5 Seconds (without alignments) 47.436 Million cell updates/sec
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/cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
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/cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*
                         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-909-122-5

US-10-050-611-4

US-10-050-611-4

US-10-050-688-5

US-10-050-688-6

US-09-777-328-8

US-09-904-090-3

US-09-904-090-3

US-09-904-090-3

US-09-908-837A-45

US-09-698-837A-41
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US-10-182-263-3
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US-10-182-263-5
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1 AGTRIKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_AA:*
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JS-09-978-9
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 303.1000-008
CURRENT APPLICATION NUMBER: US/10/050,611
CURRENT PILING DATE: 2002-01-16
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FARELSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 23
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED TITLE OF INVENTION: PEPTIDES FILE REFERENCE: 303.1000-000 CURRENT APPLICATION NUMBER: US/10/050,611 CURRENT FILING DATE: 2002-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.2e-10;
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100.0%; Pred. No. 4.2e-10
iive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: human fragment of thrombin US-10-050-611-3
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                                                                                                                  PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DAVE: 2001-07-12
PRIOR FILING DAVE: 2001-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23
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Best Local Similarity 100..
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Best Local Similarity
Matches 21; Conservē
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                                                 APPLICANT: Crowther, Roger S.
APPLICANT: Stienhery, Janet
APPLICANT: Stienhery, Janet
APPLICANT: Stienhery, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
TITLE REPERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
PRIOR APPLICATION NUMBER: US 60/219,800
PRIOR FILING DATE: 2000-07-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Peptide fragment of Thrombin US-09-909-348-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Peptide fragment of Thrombin US-09-909-122-5
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CURRENT APPLICATION NUMBER: US/09/909,122
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTUMARE: 25
LENGTH: 25
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: Stimulation Of Bone of TITLE OF INVENTION: Peptide Derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGTRYKPDEGKRGDACEGDSGGPFV 25
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Publication No. US20020187933A1
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                             Darrell H.
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APPLICANT: Carney, Darrell H.
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LENGTH: 25
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Patent No. US20020032314A1

Patent No. US20020032314A1

APPLICANT: CAREY, DARRELL H.

APPLICANT: RAMMKRISHNAN, SHYAM

TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS

TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS

CURRENT APPLICATION NUMBER: US/09/777,328

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 08/330,594

PRIOR FILING DATE: 1994-10-28
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US-09-777-328-8
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 303.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT APPLICATION NUMBER: US 60/217,583
PRIOR APPLICATION NUMBER: US 60/217,583
PRIOR PILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23
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Pred. No. 4.2e-10;
0: Mismatches 0;
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100.0%; Pre
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Patent No. US20020061852A1
                                                Sequence 8, Application US/09777328
Patent No. US20020032314A1
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 21; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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LENGTH: 23
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                                  TITLE OF INVENTION: STRUCLATION OF CARTILAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REPERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT PELING DATE: 2002-01-16
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTHARR: FASTERO for Windows Version 4.0
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APPLICANT: Crowther, Roger S.
APPLICANT: Stlernberg, Janet
APPLICANT: Stlernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
FILE REFERENCE: 3033.1003-004
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Pred. No. 4.2e-10
0; Mismatches 0
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FEATURE:
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CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FREESEQ for Windows Version 4.0
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Best Local Similarity 100.0%; P.
Matches 21; Conservative 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0%;
Matches 21; Conservative (
Stiernberg, Janet
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; OTHER INFORMATION: CONH2
US-10-050-688-6
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LENGTH: 23
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PPLICANT: MacDougall, John R
ITLE OF INVENTION: NOVEL SERINE/THREONINE PROFEIN-KINASE LIKE PROFEINS AND
ITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
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                                                                                                                                                                                            Score 114; DB 9;
Pred. No. 4.1e-08;
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Pred. No. 4.1e-08;
); Mismatches 1
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FILING DATE: 2000-04-05
FILING DATE: 2000-04-07
FILING DATE: 2000-04-07
APPLICATION NUMBER: U.S.S.N. 60/197,080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-04-13
APPLICATION NUMBER: U.S.S.N. 60/232,677
FILING DATE: 2000-09-15
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FILING DATE: 2000-04-03
APPLICATION NUMBER: U.S.S.N. 60/215,906
FILING DATE: 2000-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: U.S.S.N. 60/181,347 FILING DATE: 2000-02-09
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                                                                                                                                                                                                                                      0; Mismatches
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Publication No. US20030077697A1
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Taupier Jr., Raymond
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Gerlach, Valerie L
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                                                                                                                                                                                            80.9%;
95.2%;
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Burgess, Catherine
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95.2%;
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                                                                                                                                                                                          Query Match
Best Local Similarity 95.2
Matches 20; Conservative
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Vernet, Corine
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Best Local Similarity 95.2
Matches 20; Conservative
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PRIOR FILING DATE: 2000-1
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2
SEQ ID NO 45
LENGTH: 250
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                                                                                                     TYPE: PRT
GRGANISM: Bos taurus
US-09-898-837A-45
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CORGANISM: BOS taurus
US-09-898-837A-41
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ITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
ITLE OF INVENTION: NOCLEIC ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: c-terminal amidated fragment of human thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
                                 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES
FILE REFERENCE: 303.1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR PELICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
SPRIOR FILING DATE: 2000-07-19
SPRIOR FILING DATE: 2000-07-19
SPRIOR FILING DATE: 2000-07-19
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 9;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: AMIDATION

LOCATION: (23)...(23)

COTHER INFORMATION: valine is amidated as CONH2
US-10-050-692-6
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PRIOR APPLICATION UNMER: U.S.S.N. 60/165,986
PRIOR FILING DATE: 1999-11-17
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NG DATE: 2000-04-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: U.S.S.N. 60/181,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: U.S.S.N. 09/715,427
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Publication No. US20030077697A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGTRYRPDEGKRGDACEGDSGGPFV 25
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nupier Jr., Raymond
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Irgess, Catherine
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Best Local Similarity 92.0%;
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 20
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US-09-898-837A-45
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DB 9; Length 419;
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APPLICANT: Grinnell, Brian W
FILE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182, 263
                                                                                                                                                                                                                                                                                                                     Score 71;
                                                                   CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR PILING DATE: 2002-01.11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
LENGTH: 419
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Job time : 49.5 secs
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US-10-182-263-4
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Best Local Similarity
Matches 13; Conserv
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Pred. No. 0.05;
0; Mismatches 3; Indels
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Pred. No. 0.05
0; Mismatches
                                                                              APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruce E
APPLICANT: Grinell, Brian W
TITLE OF INVEWION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARRE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3.4 Application US/10182263
Publication No. US200300223541
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Grimell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                       Sequence 1, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION:
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ilarity 81.2%;
Conservative
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Best Local Similarity 81.2
Matches 13; Conservative
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US-10-182-263-3
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: HOI
US-10-182-263-1
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LENGTH: 419
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LENGTH: 419
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US-10-182-263-4
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Gaps

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3; Indels

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein May 12, 2003, 15:33:02; Search time 28.5 Seconds (without alignments) 84.328 Million cell updates/sec Run on:

US-09-909-348-5 Title: Perfect score:

141 1 AGTRYKPDEGKRGDACEGDSGGPFV 25 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched: 283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
-	121	85.8	622	н	TBHU	thrombin (EC 3.4.2
7	117	83.0	236	~	C42696	thrombin (EC 3.4.2
က	114	80.9	625	Н	TBBO	
4	108	9.9/	234	7	F42696	_
S	103	73.0	235	~	D42696	_
φ	103	73.0	235	~	E42696	thrombin (EC 3.4.2
7	100	70.9	236	~	142696	thrombin (EC 3.4.2
æ	66	70.2	239	7	G42696	thrombin (EC 3.4.2
6	92	65.2	617	~	S10511	_
10	92	65.2	618	ď	A35827	thrombin (EC 3.4.2
11		56.0	235	~	H42696	_
12	71	50.4	461	Н	КХНО	protein C (activat
13	70.5	50.0	264	~	S32794	4
14	67	47.5	225	~	S45356	~
15	49	47.5	417	Н	S00845	hepsin (EC 3.4.21.
16	29	47.5	1524	~	т30337	polyprotein - Afri
17	65	46.1	275	N	S40007	trypsin (EC 3.4.21
18	65	46.1	482		EXRT	coagulation factor
19	64.5	45.7	161	N	I48158	coagulation factor
20	64	45.4	191	ď	S54115	complement factor
21	64	45.4		-	DBHO	complement factor
22	64	45.4		~	B49878	coagulation factor
23	. 64	45.4		-	KXBO	protein C (activat
24	64	45.4	1004	~	T30338	oviductin (EC 3.4.
25	64	45.4	2616	~	A57096	nudel protein prec
26	63	44.7	161	~	162744	coagulation factor
27	63	44.7	461	-	JX0210	protein C (activat
.28	63	44.7	488	Н	EXHO	coagulation factor
29	62	44.0	263	-	155608	complement factor

tryptase (EC 3.4.2	protein C (activat	coagulation factor	plasmin (EC 3.4.21	tissue kallikrein	probable serine pr	limulus clotting e	t-plasminogen acti	coagulation factor	serine proteinase	coagulation factor	coagulation factor	plasma kallikrein	trypsin (EC 3.4.21	serine proteinase	trypsin-like prote	
JC4171	S18994	EXCH	PLBO	A37938	T35195	A23689	UKHUT	184621	A30100	JQ0419	EXBO	KOHUP	TRCY1	S55493	865465	
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274	461	475	812	260	285	375	562	282	392	459	492	638	237	250	254.	
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62	62	62	62	61.5	61	61	61	60.5	60.5	60.5	60.5	60.5	9	9	9	
30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45	
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ALIGNMENTS

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SULT	

TBHU thrombin (EC 3.4.21.5) precursor [validated] - human N;Alternate names: coagulation factor II N;Contains: prothrombin

C;Species: Homo sapiens (man)
C;Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
C;Accession: A23351; A00914; B00914; A37549; A37550; I51952
R;Degen, S.J.F.; Davie, E.M.
Bitochemistry 26, 6165-6177, 1987
A;Title: Noclectide sequence of the gene for human prothrombin.
A;Reference number: A29351; MUID:88077877; PMID:2825773

A; Accession: A29351

A; Molecule type: DNA

A; Residues: 1-622 CDEG>
A; Cross-references: GB:M17262; GB:M33691; NID:g558069; PIDN:AAC63054.1; PID:g339641
R; Degen. S.J.F.; Macdillivray, R.T.A.; Davie, E.W.
R; Degen. S.J.F.; Macdillivray, R.T.A.; Davie, E.W.
A; Degen. S.J.E.; Macdillivray, R.T.A.; Davie, E.W.
A; Title: Characterization of the complementary deoxyribonucleic acid and gene coding A; Reference number: A00914; MUID:83231469; PMID:6305407

A; Accession: A00914

A;Molecule type: mRNA A;Residues: 8-163,'N',165-622 <DE2> A;Cross-references: GB:V00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344 A; Accession: B00914
A; Molecule type: DNA
A; Residues: 188-311 <DE3>
R; Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A; Reference number: A37549; MUID:77193964; PMID:266717

A; Accession: A37549
A; Molecule type: protein
A; Reaidues: 44-118, 'N', 120,'S', 122-163,'I', 165-175,'A', 177-182,'T', 184-193,'MV', 196-3
A; Reaidues: 44-118, 'N', 120,'S', 122-163,'I', 165-175,'A', 177-182,'T', 184-193,'MV', 196-3
B; Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.
J. Blol. Chem. 252, 4942-4957, 1977
A; Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A; Reference number: A37550; MUDE:77207112; PMID:873923

A;Molecule type: protein A;Residues: 315-334, N',336-348, N',350-368, N',370-397, N',399-413, N',415-484, N',4 R;Rabiet, M.J.; Blashill, A.; Furie, B.C. J. Blol. Chem. 261, 13210-13215, 1986 A;Reference number: A37551; MUID:87008532; PMID:3759958

A;Contents: annotation; activation cleavages R;MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C. Ann. N. Y. Acad. Sci. 485, 73-79, 1986

A;Title: Recombinant genetic approaches to functional mapping of thrombin. A;Reference number: I51952; MUID:87182874; PMID:3471151

A:Status: translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-2,'RI',5-100 <RES>

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Rybark, C. H.; Tullnaky, A.
Blochemistry 25, 3977-3982, 1986
A/Tille: Three-dimensional structure of the kringle sequence: structure of prothrombi A/Tille: Three-dimensional structure of the kringle sequence: structure of prothrombi A/Feference number: A37553; MUID:86296631; PMID:3741841
A/Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms R/IrWin, D.M.; Ahern, K.G.; Pearson, G.D.; MacGillivray, R.T.A.
Blochemistry 24, 6854-6861, 1985
A/Title: Characterization of the bovine prothrombin gene.
A/Reference number: A37554; MUID:86077733; PMID:3000440
A/Contents: annotation; gene structure
R/MacGillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A/Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
A/Reference number: 146045; MUID:81054926; PMID:6254059
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C;Comment: The prothrombin precursor is synthesized in the liver.
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Reywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; gl F;124/Domain: signal sequence #status predicted Fil-14/Domain: gla domain mology cGLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Molecule type: protein
A; Residues: 318-325, 333-338, 'X', 340; 367-374; 481-484, 'X', 486-488; 515-522 < PEJ>
A; Residues: 318-325, 333-338, 'X', 340; 367-374; 481-484, 'X', 486-488; 515-522 < PEJ>
C; Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fil C; Comment: Prothrombin is activated on the surface of a phospholipid membrane that bit tivation peptide and cleaves the remaining part into light and heavy chains. The acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 466-599, 'N', 601-625 < MA2>
A; Residues: 466-599, 'N', 601-625 < MA2>
A; Residues: 466-599, 'N', 601-625 < MA2>
A; Cross-references: EMBL:V00135; NID:9772; PIDN:CAA23451.1; PID:9808945
B; Pejler, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Blochem. 227, 102-107, 1995
A; Title: Identification of the proteolytic thrombin fragments formed after cleavage A; Reference number: 867518; MUID:95154277; PMID:7851376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 44-287,'N',289-352,'E',354,'Q',356-548,'ND',551-599,'N',601-625 <WAG>
A;Note: the evidence for 231-Ser is strong
A;Note: disulfide bonds and carbohydrate binding sites were determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;MacGillivray, R.T.A.; Davie, E.W.
Blochemiatry 23, 1636-1634, 1984
A:Title: Characterization of bovine prothrombin mRNA and its translation product.
A:Reference number: A00915; MUID:84203525; PMID:6326805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys, H.
in Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker,
A;Reference number: A37552
                                                                                                                                                                                                                                        #text_change 18-Jun-1999
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F;200-317/Domain: activation peptide 2 #status experimental <FR2>
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                                                                                                                                                              C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change
C;Accession: 802537; A00915; A37552; 146045; 867518
R;Irwin, D.W.; Robertson, K.A.; Macdillivray, R.T.A.;
J. Mol. Biol. 200, 31-45, 1988
A;Title: Structure and evolution of the bovine prothrombin gene.
A;Reference number: 802537; MUID:88245190; PMID:3379642
A;Accession: 802537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-230,'H',232-625 <
A;Note: 600-Asn was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-625 <IRW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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thrombin (EC 3.4.21.5) B chain - rabbit (fragment)
C15pecies: Oryctolagus cuniculus (domestic rabbit)
C15pate: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C15Accession: C42696
C16Accession: C42696
C16Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; CLOSS -references: GDB:119894; OMIM:176930
A; Map position: 11p11-11q12
A; CLOSS -references: GDB:119894; OMIM:176930
A; Map position: 11p11-11q12
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Seywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
F; 1-24/Domain: aignal sequence #status predicted <PRO>
F; 25-43/Domain: aignal sequence #status predicted <PRO>
F; 25-43/Domain: propeptide #status experimental <AMT>
F; 24-622/Product: prothrombin #status experimental <AMT>
F; 44-622/Product: prothrombin #status experimental <AMT>
F; 44-327/Domain: activation peptide #status experimental <AMT>
F; 44-327/Domain: kringle homology <ARR>
F; 100-186/Domain: kringle homology <ARR>
F; 28-363/Product: thrombin light chain #status experimental <AMCH>
F; 36-622/Product: thrombin light chain #status experimental <AMCH>
F; 36-622/Product: thrombin light chain #status experimental <AMCH>
F; 36-62, 90-103; 108-186; 129-169; 157-181; 213-291; 234-274; 262-286/Disulfide bonds: #status F; 36-65; 90-103; 108-186; 129-169; 157-181; 213-291; 234-274; 262-286/Disulfide bonds: #status predicted
F; 316-65, 90-103; 108-186; 129-169; 157-181; 213-291; 234-274; 262-286/Disulfide bonds: #status predicted
F; 316-826, 550, 564-594; Prisulfide bonds: #status predicted
F; 316/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 568/Active site: Ser #status experimental
F; 568/Active site: Ser #status experimental
A;Cross-references: GB:M33031; NID:g190723; PIDN:AAA60220.1; PID:g190724
C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibri
C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
C;Comment: Prededelther by factor Xa or thrombin; the cleavage into light and heavy chai
ter 314-Arg, are released in natural blood clotting.
C;Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
C;Comment: The prothrombin precursor is synthesized in the liver.
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Pred. No. 8.3e-09;
1; Mismatches 0
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Mismatches

100.08; Pr.

Query Match 85.8 Best Local Similarity 100. Matches 21; Conservative

553 YKPDEGKRGDACEGDSGGPFV 573

5 YRPDEGKRGDACEGDSGGPFV 25

õ

167 YKPEEGKRGDACEGDSGGPFV 187

셤

83.0%; 95.2%;

Query Match 83.0 Best Local Similarity 95.2 Matches 20; Conservative

Tue May 13

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r42696
through (EC 3.4.21.5) B chain - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: 142696
B;Banfield, D.K.; Macdillivray, R.T.A.
B;Banfield, D.K.; Macdillivray, R.T.A.
B;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Reference number: A42696; MUID:92212913; PMID:1557383
A;Accession: 142696
A;Status: preliminary: not compared with conceptual translation
A;Mesidues: 1-236 CBAN>
A;Cross-references: GB-M81333
A;Cross-references: GB-M81333
                                                                                                                      C; Species: Gekko gecko (toka)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C; Accession: E42696
C; Accession: E42696
R; Banfield, D.K.; MacGillivray, R.T.A.
R; Banfield, D.K.; MacGillivray, R.T.A.
A; Title: Partial characterization of vartebrate prothrombin cDNAs: amplification and A; Reference number: A42696; MuID:92212913; PMID:1557383
                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: mRNA
A;Residues: 1-235 <BAN>
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Ostobe

Cispecies: Oncorhynchus mytiss (rainbow trout)

Cispecies: Oncorhynchus mytiss, 89, 2779-2783, 1992

A; Raference number: A42696; MulD:92212913; PMID:1557383

A; Accession: G4266

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-239 <BAN>

A; Cross-references: GB:M81398; NID:9213486; PIDN:AAA49433.1; PID:9213487
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C;Superfamily: thrombin: Gla domain homology; kringle
C;Keywords: hydrolase; serine proteinase
C;Keywords: tydrolase; berine proteinase
F;1-226/Domain: trypsin homology (fragment) <TRY>
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Pred. No. 7.1e-07;
2; Mismatches 2;
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Pred. No. 1.8e-06;
2; Mismatches 2;
                                                                                                           thrombin (EC 3.4.21.5) B chain - tokay (fragment)
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1 Similarity 81.0%;
17; Conservative
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81.0%;
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nes 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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Matches
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F;214-292/Domain: kringle homology <KR2>
F;318-366/Product: thrombin light chain #status experimental <LCH>
F;367-616/Product: thrombin heavy chain #status experimental <HCH>
F;367-616/Domain: trypsin homology <TRX>
F;367-616/Domain: trypsin homology <TRX>
F;50.51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;61-66,91.104,109-187,130-170,138-182,214-222,235-275,23-287,339-485,394-410,539-553,571,20,144,419/Binding site: carbohydrate (Asn) (covalent) #status experimental F;409,465,571/Active site: His, Asp, Ser #status experimental
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C;Species: Gallus gallus (chicken)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: 42696
R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin CDNAs: amplification and sA;Accession: 42696; MUID:92212913; PMID:1557383
A;Accession: b42696
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <-BAN>
A;Cross-references: GB:M81391
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Superfamily: trypsin homology (framment) <-TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombin (EC 3.4.21.5) B chain - Cynops pyrogastor (fire-bellied newt) (fragment) C. Species: Cynops pyrogastor (fire-bellied newt) C. Species: Cynops pyrogastor (fire-bellied newt) C. Dec-1997 #sequence_revision 19-bec-1997 #text_change 17-Mar-1999 C. Accession: F42696 C. T. O. S. A. B9, 2779-2783, 1992 A. Tille: Partial characterization of vertebrate prothrombin cDNAs: amplification and s. Note: sequence not A. Accession: F42696 A. Accession: F42696 A. Status: preliminary: nucleic acid sequence not shown; not compared with conceptual the A. Molecule type: mRNA A. Molecule types: MRNA A. M
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                                                                                                                                                                                                                                                                                                                    Length 625;
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Pred. No. 1.4e-07;
0; Mismatches 2;
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Pred. No. 7.1e-07;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                 Score 114; DB 1;
Pred. No. 5.5e-08;
0; Mismatches 1.
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95.2%;
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81.0%;
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Best Local Similarity 90.5%;
Matches 19; Conservative
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Best Local Similarity 95.2
Matches 20; Conservative
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Best Local Similarity 81.0
Matches 17; Conservative
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RESULT 11
H42696
thrombin (EC 3.4.21.5) B chain - white sturgeon (fragment)
C; Species: Acipenser transmontanus (white sturgeon)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C; Accession: H42696
N; Banfield, D.K.; Macdillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A; Reference number: A42696; MUID:92212913; PMID:1557883
A; Accession: H42696
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A; Molecule type: mRNA
A; Molecule type: mRNA
A; Across: references: GB MB1399
A; Cross: references: GB
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F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;51-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-54
F;403,459,565/Active site: His, Asp, Ser *status predicted
                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain C57BL/6
A; Note: the data were obtained from females resulting from the cross of M. domesticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Reference number: A42696; MUID:92212913; PMID:1557383
A;Accession: A42696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C; Superfamily: thrombin; Gla domain homology; craboxyglutamic acid; glycoprotein; E; 1-24/Domain: signal sequence #status predicted <SIG> F; 2-4/Domain: propeptide #status predicted <PRO> F; 25-43/Domain: gla domain homology <GLA> F; 28-88/Domain: Gla domain homology <GLA> F; 28-88/Domain: Gla domain monology <GLA> F; 109-18/YDomain: kringle homology <RRI> F; 109-18/YDomain: kringle homology <RRI> F; 25-293/Domain: kringle homology <RRI> F; 215-293/Domain: kringle homology <RRI> F; 215-293/Domain: kringle homology <PRI> F; 215-29
                                                     prothrombin and localization
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    DNA Cell Biol. 9, 487-498, 1990
A;Title: Characterization of the cDNA coding for mouse E
A;Reference number: A35827; MUID:91025551; PMID:2222810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein C (activated) (EC 3.4.21.69) precursor - human N; Alternate names: autoprothrombin IIA; plasma protein
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5.9e-05;
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Pred. No. 0.0015;
3; Mismatches
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Pred. No. 5.9e-
3; Mismatches
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61.9%;
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76.2%;
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Best Local Similarity 76.2°
Matches 16; Conservative
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Cross-references: GB:M81394
                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-618 <DEG>
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A; Residues: 44-58 <hr/>
A; Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
R; Banfield, D.K.; MadGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A; Reference number: A42696; MUID:92212913; PMID:1557383
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C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 03-May-2002
C;Accession: A33827; A42696; S12081
R;Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.
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;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5
;402,458,564/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
R;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A;Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A;Reference number: A60576; MUID:90091942; PMID:2293980
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Keywords: hydrolase; serine proteinase F;1-226/Domain: trypsin homology (fragment) <TRY>
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C;Dactes (7-May-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
C;Daccession: S10511; A0576; B42696
R;Dihanich, M.; Monard, D.
Nucleid Acids Res. 18, 4251, 1990
A;Title: CDNA sequence of rat prothrombin.
A;Title: CDNA sequence of rat prothrombin.
A;Reference number: S10511; MUID:90332426; PMID:2377469
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                              Length 239
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Pred. No. 5.9e-05;
3; Mismatches 2;
                                                                                                                                                                                         Score 99; DB.2; Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                      2; Mismatches
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thrombin (EC 3.4.21.5) precursor - rat
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                                                                                                                                                                                                                                                                                                                                                                              5 YKPDEGKRGDACEGDSGGPFV 25
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Best Local Similarity 76.2%;
Matches 16; Conservative
                                                                                                                                                                                    Query Match 70.2%;
Best Local Similarity 81.0%;
Matches 17; Conservative
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Residues: 383-617,'E' <BAN>
Cross-references: GB:M81397
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A; Residues: 1-617 <DIH>
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C; Accession: S32794
R; Ikeda, M.; Yaginuma, T.; Kobayashi, M.; Yamashita, O.
Comp. Blochem. Physiol. B 99, 405-411, 1991
A; Title: CDNA cloning, sequencing and temporal expression of the protease responsible A; Reference number: S32794; MUID: 92111263; PMID:1764920
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                                                         (partial) #status atypical
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C;Date: 07-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 11-May-2000
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C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
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A;Experimental source: Alzhelmer's disease patient brain cortex
                                                                                                                                                                                                                Gaps
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R; Dihanich, M.; Spiess, M.
Biochim. Biophys. Acta 1218, 225-228, 1994
A; Title: A novel serine proteinase-like sequence from human brain.
A; Reference number: $45356; MUID:94289486; PMID:8018728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable serine proteinase (EC 3.4.21.-) ACO - human (fragment)
                                                                                                                                   Length 461
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                       Ser #status predicted
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Pred. No. 0.024;
2; Mismatches 2;
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0.063;
                                                                                                                                   DB 1;
0.035;
               F;253,299,402/Active site: His, Asp, Ser #status p
F;371/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                               Score 71; DB :
Pred. No. 0.03:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin-like proteinase (EC 3.4.21.-) - silkworm
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Pred. No. 0.063
3; Mismatches
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                                                                                                                                   50.4%;
81.2%;
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                                                                                                                                                                                                                                                                                                                        392 GDRODACEGDSGGPMV 407
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Best Local Similarity 64.03
Matches 16; Conservative
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                                                                                                                               Query Match 50.4
Best Local Similarity 81.2
Matches 13; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                 10 GKRGDACEGDSGGPFV 25
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S00845
hepsin (EC 3.4.21.-) - human
C;Species: Homo sapiens (man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA A; Residues: 1-264 <IKE>
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A:Status: preliminary
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:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/t
:106-111/Disulfide bonds: #status predicted
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A; Residues: 'Q', 107-461 <FOS2>
A; Cross-rences: 'Q', 107-461 <FOS059; NID:g190322; PIDN: AAA60164.1; PID:g190323
A; Cross-rences: GB: K02059; NID:g190322; PIDN: AAA60164.1; PID:g190323
B; Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
Nucleic Acids Res. 13, 5233-5247, 1985
A; Title: The structure and evolution of a 461 amino acid human protein C precursor and i
A; Reference number: A23789; MUID: 85269639; PMID: 2991859
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F;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;139,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
, vate: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
;Accession: A22331; A25426; A21781; A23789; A00927
;Foster, D.C.; Yoshitake. c · Part.
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A;Molecule type: DNA
A;Residues: 1-445,'L',446-461 <PLU>
A;Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332
                                                                                                                                                                                                                                                                                                        A.Molecule type: DNA
A.Residues: 1-461 <FOSI>
A.Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334
A.Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334
R.Plutzky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A.Title: Evolution and organization of the human protein C gene.
A.Reference number: A25426; MUID:86120978; PMID:3511471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1-461 <BEC>
Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
                                                                                                                   R.Foster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985.
A.Title: The nucleotide sequence of the gene for human protein C.
A.Reference number: A22331; MUID:85270390; PMID:2991887
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roc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

ritle: Characterization of a cDNA coding for human protein C. Reference number: A21781; MUID:84272714; PMID:6589623

Accession: A21781
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200-461/Product: protein C heavy chain #status predicted <HCH
200-211/Domain: activation peptide #status experimental <APT>
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               C; Species: Homo sapiens (man)
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Riceytus, S.P.; Lob, K.R.; Hagen, F.S.; Kurachl, K.; Davle, E.W.
Blochemistry 27, 1067-1074, 1988
A;Title A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom A;Reference number: S00845; MUID:88209431; PMID:2835076
A;Accession: S00845
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A;Residues: 1-417 <LEF>
A;Residues: 1-417 <LEF>
A;Cross_references: EMBL:X07732; NID:932063; PIDN:CAA30558.1; PID:932064
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999 sion: S00845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: HPN; TMPRSS1; hepsin
A; Cross-references: GDB:135685; OMIM:142440
A; Map position: 1941-119413.2
C; Superfamily: hepsin; trypsin homology
C; Keywords: hydrolase; llver; serine proteinase; transmembrane protein
F; 23.45.Domain: transmembrane #status predicted <TMN>
F; 163-400/Domain: trypsin homology <TRY>
F; 168-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F; 108-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F; 203,257,353/Active site: His, Asp, Ser #status predicted
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Search completed: May 12, 2003, 15:39:44 Job time: 28.5 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 12, 2003, 15:32:07 ; Search time 14.5 Seconds (without alignments) 71.511 Million cell updates/sec

US-09-909-348-5 141 1 AGTRYKPDEGKRGDACEGDSGGPFV 25

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum.Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ption	homo sapten	bos taurus	rattus norv	mus musculu	macaca mula	homo sapien	bombyx mori	drosophila	homo sapien	oryctolagus	homo sapien	mus musculu	homo sapien	homo sapten	canis famil		felis silve	equus cabal	anopheles g	mus musculu	homo sapten	sus scrofa	рошо	homo sapien	sus scrofa	bos taurus	bos taurus	homo sapien	drosophila	drosophila	mus musculu	homo sapien	homo sapien
Description	P00734	P00735	P18292	P19221	028506	P04070	007943	P54630	09bqr3	028661	Q9h2r5	035453	P05981	Q9ukr3	028278	028315	028412	028380	P35037	Q9er04	Q9h3s3	09g1p2	09u152	P00746	P51779	P00745	028198	P56730	P98159	P54627	P33587	P00742	09p0g3
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% Query Match	85.8	6.08	65.2	65.2	50.4	50.4	50.0	49.6	48.6	48.2	47.5	•	47.5	46.5	46.1	46.1	46.1.	46.1	46.1	46.1	46.1	46.1	45.7	45.4	45.4	45.4	45.4	45.4	45.4	44.7	44.7	44.7	44.0
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CFAD_RAT MCT6_RAT PRTC_RAT FR10_CHICK HGFA_MOUSE PINN_BOVIN ESTA_CANFA TEST_MOUSE TEST_MOUSE CFAI_MOUSE TRY4_LUCCU
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Cera E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT FRANKFURT.
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                                                                                                                                                       thrombin.
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Type 3 (157 Glu leads to Lys) and the localization of a third
thrombin cleavage site.";

L. THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,

C. THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

C. THROMBIN THROMBONDOULN, PROTEIN C.

C. TATALYTIC ACTIVITY: Preferently PROTEIN C.

C. TATALYTIC ACTIVITY: Preferently FROME And B.

C. TOMPORTION TO FIBRIN AND ACTIVATES FOUND IN PLASMA.

C. TOMPORTION THE GRAMA-CARBOXYCLOTHAT. RESIDUES, WHICH BIND CALCIUM IONS,

RESULT FROM THE CARBOXYCLOTHATL RESIDUES, WHICH BIND CALCIUM IONS,

C. THE MODIFIED RESIDUES

C. THE MODIFIED RESIDUES

C. THE MODIFIED RESIDUES

C. CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
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MISCELLANBOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A

MISCELLANBOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A

PACOSPHOLIPID MEMBRANE THAT BINDS THE ANTON END OF PROTHROMBIN 6

PACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES

THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT 6

HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR

V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANDOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN NATURAL BLOOD CLOTTING.
MISCELLANDOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROFHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
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Míyata T., Morita T., Inomoto T., Rawauchi S., Shirakami A.,
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MEDLINE-92256895; Pubmed-1349838;
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MEDLINE-92378975;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos
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MEDLINE-91311686; PubMed-1856869;
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                   Length 622;
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                                      2.6e-09;
                     DB 1;
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01-APR-1990 (Rel. 14, Last sequence update)
02-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
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0; Mismatches
                                                                                                                                                                                                                                              625 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92190185; Pubmed-1547238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84203525; PubMed-6326805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 23:1626-1634(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prothrombin fragment 1.";
Biochemistry 25:3977-3982(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Biol. 220:481-494(1991).
                                                                                                                      553 YKPDEGKRGDACEGDSGGPFV 573
                                                                                                  YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. 200:31-45(1988)
                                                       Conservative
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          taurus (Bovine)
               Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resolution.
                                                                                                                                                                                                                                            THRB_BOVIN
P00735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product
                                                                                                                                                                                                                        THRB_BOVIN
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                                                                                                                                                                                                     RESULT 2
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MEDLINE-8607733; Pubmed-3000440;

RA MEDLINE-8607733; Pubmed-3000440;

RIWAIN D.M. Ahern K.G., Pearson G.D., McGillivray R.T.A.;

"Characterization of the bovine prothrombin gene.";

Blochemistry 24:6854-6861(1985).

-I- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,

AND, IN COMPLEX WITH THROMBOWDOLLIN, PROTEIN C.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Gly; activates

-I- SIDECLIDIAR LOCATION: Extracellular.

-I- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.

-I- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.

-I- PTM: THE GAMMA-CARBOXYLGUTAMYL RESIDUES WITH MODIFIED RESIDUES

-I- PTM: THE GAMMA-CARBOXYLGUTAMYL RESIDUES WITH MODIFIED RESIDUES

-I- PTM: THE GAMMA-CARBOXYLGUTAMYL RESIDUES WITH MODIFIED RESIDUES

-I- PTM: THE VITAMIN TO PERDENDENT CARBOXYLASE. THE MODIFIED RESIDUES

-I- MISCELLANBOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PROSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN E CLEAVES THE REMAINING PART INTO LIFE OF THE ACTIVATION PROCESS STARTS SLOWIX BECAUSE FACTOR THE ACTIVATION PROFILE A CHEAVES THE REMAINING PART INTO LIFE OF THE MODIFIED FACTOR.

--- THE ACTIVATION PROPILE INTIBAL, SMALL AMOUNTS OF THE MODIFIED AMENDED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
MEDLINE-97102783; PubMed-8947023;
van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweller C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J., Martin P.D., Edwards B.F.P., Bode W.:
"Refined 2.3 A X-ray crystal structure of bovine thrombin complexes formed with the benzamidine and arginine-based thrombin inhibitors NAPAP, 4-TAPAP and MQPA. A starting point for improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huber R., Bode W.; "Structure of the thrombin complex with triabin, a lipocalin-like exosite-binding inhibitor derived from a triatomine bug."; Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The ornithodorin-thrombin crystal structure, a key to the TAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF COMPLEX WITH TRIABIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY FACTOR XA.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 KRINGLE DOMAINS
DATABASE: NAME-ProZyme technical fact sheet;
WMW-"http://www.prozyme.com/technical/thrombindata.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                   NAPAP, 4-TAPAP and MOPA. A starting antithrombotics.";
                                                                                                                                                                                                                                                                      Mol. Biol. 226:1085-1089(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98004486; PubMed-9342325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; V00135; CAA23451.1; -. EMBL; J00041; AAA30781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 15:6011-6017(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1BBR; 31-JAN-94
1ETR; 31-JAN-94
1ETS; 31-JAN-94
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PIR; S02537; S02537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huber R
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556 YKPGEGKRGDACEGDSGGPFV 576
                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THROMBIN.
                                                                                                                                                                                                                                                     TISSUE-Liver;
                                                                     01-NOV-1990
                                                 THRB_RAT
 셤
                                                                                                                                                                                                                                                                                                                                                                                           Acute phase; Liver
                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
BLOOD COSQUIATION; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin R; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Live Hydrolase; Serine protease; Kringle; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE (FRAGMENT 1)
ACTIVATION PEPTIDE (FRAGMENT 2)
THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 114; DB 1; Length 62
Pred. No. 2.4e-08;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (BY THROMBIN).
CLENVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAMMA-CARBOXYGLUTAMIC
GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-CARBOXYGLUTAMIC GAMMA-CARBOXYGLUTAMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTHROMBIN.
                                                                                                                                                                                                                                                                                                        Tryp_SPc; 1.
1; GLU_CARBOXYLATION; 1.
1; KRINGLE_1; 2.
0; KRINGLE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRINGLE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRINGLE 2
                                                                                                                                                                             InterPro; IPR003966; Prothrombin:
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                           nterPro; IPR002383; GLA_blood.
nterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                         CHYMOTRYPSIN
                                                                                                                                                                                                                                                                      PRO1505; PROTHROMBIN, D0000395; Kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.9%;
llarity 95.2%;
Conservative
                                                                                                                                                                                                                   Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                   GLABLOOD.
                                                                                                                                                                                                                                                              KRINGLE
                                                                                                                                                                                                           i; kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
60
63
64
70
73
                                                                                                                    17-JUN-98.
16-FEB-99.
                                                                                                        06-MAY-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Owery Match.
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                          PS50070;
                                        -MAY-
                                                                                                                                                                                                                                          RINTS; PR00722;
                                                                                                                                                                                                                                                                       PRINTS; PR01505
                                                                                                                                                                                                          fam; PF0005
                                                                                                                                        MEROPS; S01.
                                                                                                                    1AOH;
1AVG;
                                    2SPT;
                                                 1MKW;
                                                                     LTBO
                             PF2
                                                                                                                                                                                                                                                                                           SMART; SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
ACT_SITE
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                               ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                       ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4OD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                         PDB;
                                    PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                             PDB;
                            DB;
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RA Banfield D.K., Macgillitray R.T.

Rapited D.K., Macgillitray R.T.

Rapited D.K., Macgillitray R.T.

Rapited Characterization of vertebrate prothrombin cDNAs:

multification and sequence analysis of the B chain of thrombin from nine different species."

RL

Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

C. - FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER RG & LYS, CONVERTS CONVERTS WIN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER RG & LYS, CONVERTS C.C.

- AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

- TOTALITICA ACTIVITY: Preferential cleaves fibrinopeptide A and B.

C. - PTH: THE GAMMA-CARBOXYCLATION OF GLUTAWYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAWYL RESIDUES BY A MICROSOMAL ENTANE, THE VITAMIN R-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION OF PROTHROMBIN TO THROMBIN.

- PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & PROCESS THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF MUDDALIN.

- THEAVY CHAINS. THE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF MUDDALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                       01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (RC 3.4.21.5).
                                                                       617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=9033426; PubMed=2377469;
Dibanich M., Monard D.;
"cDNA sequence of rat prothrombin.";
Nucleic Acids Res. 18:4251-4251(1990).
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chymotrypsin GLA_blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kringle.
Prothrombin
                                                                                                                                       (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE OF 383-617 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X52835; CAA37017.1; -. EMBL; M81397; AAA42240.1; -. PIR; S10511. S10511. HSSP: P00734; 1UVS. MEROPS; S01.217; -.
                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314;
InterPro; IPR002383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000001;
InterPro; IPR003966;
RESULT 3
THRE RAT
THRE RAT
THRE RAT
THRE RAT
DD DT 01-N
DD 01-
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Gaps

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STANDARD;

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                     Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G., Fitzgibbon J.J., Pal J.-A., Chapman V.M., Elliott R.W.; "Characterization of the cDNA coding for mouse prothrombin and localization of the gene on mouse chromosome 2."; DNA Cell Biol. 9:487-498(1990).
                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
1-NOV-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                                                   STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-91025551; PubMed-2222810;
                                                                                                                                                                                                                                                                    SEQUENCE OF 384-618 FROM N.A.
                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                PISSUE-Liver;
                                                                01-NOV-1990
01-NOV-1990
                                             THRB_MOUSE
                                                                                                            OR CF2
                                   THRB_MOUSE
                                                        acid; Acute phase; Liver;
                                                                                                                                            PROSITE; PSO0021; RRINGLE_1; 2.
PROSITE; PS50070; RRINGLE_2; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Live Hydrolase; Serine protease; Kringle; Signal.
                                                                                                                                                                                                                                                                                                                                         CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                  ACTIVATION PEPTIDE (FRAGMENT 1).
ACTIVATION PEPTIDE (FRAGMENT 2).
THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.2%; Score 92; DB 1; Length 617; 76.2%; Pred. No. 2.5e-05; 1ve 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAMMA-CARBOXYGLUTAMIC ACID. GAMMA-CARBOXYGLUTAMIC ACID.
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                                                                                                                         SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00021; KRINGLE_1; 2.
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BY SIMILAR BY SIMILAR
InterPro; IPR001254; Ser_protease_Try
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00051; Kringle; 2.
Pfam; PF00069; 'trypsin; 1.
Pfam; PF00594; gla; 1.
                                                 PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLCOD.
PRINTS; PR000018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 2.
SWART; SM00069; GLA; 1.
SWART; SM00020; TRYP_SPC; 1.
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Best Local Similarity
Tabes 16; Conserve
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617 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
BY FACTOR XA.
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InterPro; IPR002383; GLA_blood.
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EMBL; M81394; AAA40435.1; -.
PIR; A35827; A35827.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
GRAMA-CARBOXYGLUTAMIC ACID.
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THROMBIN HEAVY CHAIN (B)
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KRINGLE 2.
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PS00011; GLU_CARBOXYLATION; 1.
PS00021; KRINGLE_1; 2.
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                                InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF000894; gla; 1.
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InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
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PRINTS; PR00001; GLABLOOD.
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PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 2.
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SMART; SM00130; KR; 2.
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618 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-94318474; PubMed-8043441; Murakawa M., Harada M., Niho Y.; Murakawa M., Okamura T., Kamura T., Kurolwa M., Harada M., Niho Y.; "A comparative study of partial primary structures of the catalytic
                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
Vitamin K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Butherla; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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N'LINARIA (GLCNAC. . ) (POTENTIAL)
N'LINKED (GLCNAC. . ) (POTENTIAL)
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HSSP; P04070; 1PCU.
MEROPS; S01.218; -.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SWART; SW000020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LHS; PARTIAL.
PROSITE; PS00135; TRYPSIN_HS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SRR; 1.
Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
NON_TER
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Pred. No. 0.0053;
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                                                         161 AA
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                                                            STANDARD;
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Score 92; DB 1; Length 618 Pred. No. 2.5e-05; 3; Mismatches 2; Indels

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Similarity 16;

65.2%;

EMBO J. 15:6822-6831(1996).

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MEDLINE-85269639; PubMed-2991859;
Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R.,
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"The 2.8 A crystal structure of Gla-domainless activated protein C.";
PRTC_HUMAN STANDARD; PRT; 461 AA.
P04070; Q16001; Q15190; Q15189;
01-NOV-1986 (Rel. 03, Last sequence update)
01-NOV-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97157472; PubMed-9003757; Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmon C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi
Nickerson D.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                Homo saplens (Human).
Bustayota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi; Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90293094; PubMed-1694179; Miletich J.P., Broze G.J. Jr.; "Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fisher C.L., Greengard J.S., Griffin J.H.; Models of the serine protease domain of the human antithrombotic plasma factor activated protein C and its zymogen."; Protein Sci. 3:588-599(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harris R.J., Ling V.T., Spellman M.W.; "O-linked fucose is present in the first epidermal growth factor domain of factor XII but not protein C."; J. Biol. Chem. 267:5102-5107(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                    "The structure and evolution of a 461 amino acid human protein of precursor and 11s messenger RNA, based upon the DNA sequence of cloned human liver colons.":
Nucleic Acids Res. 13:5233-5247(1985).
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cysteine sites.";
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MEDLINE-86120978; Pubmed=3511471;
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MEDLINE-84272714; PubMed-6589623;
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MEDLINE-93190290; PubMed-8446940;
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MEDLINE-92305321; PubMed-1611081;
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MEDLINE-93250852; PubMed-1301959;
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MEDLINE-92380660; Pubmed-1511988;
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Hum. Genet. 89:683-684(1992)
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Blood 78:890-894(1991).
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CONFLICT
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitelilin-degrading protease precursor (EC 3.4.21.-) [Contains: Alpha-VIN protease; Beta-VIN protease]
                     VARIANT SER-334.

MEDLINE-92276939; PubMed-1593215;
Yamanoto K., Matsushita T., Sujdura I., Takamatsu J., Iwasaki E.,
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Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426
MEDLINE-94122329; PubMed-8292730;
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"Genetic mutations in ten unrelated American patients with
"Genetic mutations in ten unrelated American
"Genetic repet in protein C deficiency.";
Blood Coagul. Fibrinolysis 4:791-796(1993).
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                                                                                                                         VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
MEDLINE-93313192; Pubmed-8324221;
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lood Coagul. Fibrinolysis 4:345-347(1993).
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MEDLINE-94001606; Pubmed-8398832;
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Mutat. 1:491-500(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE.
STRAIN-Shunrel X Shogetu; TISSUE-Egg;
IKeda M., Sasaki T., Yamasahita O.;
IKeda M., Sasaki T., Yamasahita O.;
Ikeda M., Sasaki T., Yamasahita O.;
Insect Biochem. 20:725-734(1990).
Insect Biochem. 20:725-734(1990).
Insect Biochem. 20:725-734(1990).
ITEMICATION: RESPONSIBLE FOR THE DEGRADATION OF VITELLIN IN EGGS AT THE HEAD PICHENTARION STAGE.
I- DEVELOPMENTAL STAGE: APPEARED ON EGG DAY 7.5, BECAME MORE ACTIVE ON DAY 8-8.5 AND DISAPPEARED ON DAY 9.5.
I- PTM: CLEAVAGE AFTER ARG-27 LEADS TO BETA-VTN PROTEASE AND SUBSEQUENT CLEAVAGE AFTER ARG-89 LEADS TO ALPHA-VTN.
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                                                                                                                                                                                                                                                           Ikeda M., Yaginuma T., Kobayashi M., Yamashita O.;
"cDNA cloning, sequencing and temporal expression of the protease
responsible for vitellin degradation in the silkworm, Bombyx mori.";
Comp. Biochem. Physiol. 998:405-411(1991)
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ALPHA-VIN PROTEASE CHAIN 2 (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                 Hexapoda;
Bombyx mori (Silk moth).
Būkaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysla; Bombycoldea; Bombycidae; Bombyx.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                    STRAIN-N4; TISSUE-Egg;
MEDLINE-92111263; PubMed-1764920;
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SMOSITE; PS50240; TRYPSTR_DOM; 1.
PROSITE; PS00134; TRYPSTR_HS; 1.
PROSITE; PS00135; TRYPSTR_SER; 1.
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PRINTS; PR00722; CHYMOTRYPSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D16232; BAA03757.1; -. EMBL; D16233; BAA03758.1; -. PIR; S32794; S32794; HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 64.0
nes 16; Conservative
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161
251
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.113:
                                                                                                                   NCBI_TaxID=7091;
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rryz_droer

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vitamin-K dependent protein C precursor (BC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERIME PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
WHINKED (GLCNAC. . .) (POTENTIAL).
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutharla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
SIMILARITY).
SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                    SEQUENCE FROM N.A. Fawlings N.D., Barrett A.J.; Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.; "Cloning, sequencing and expression of marapsin, a human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; DB 1; Length 290; 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68.5; Di
Pred. No. 0.02:
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pram; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_EIS; 1.
PROSITE; PS00135; TRYPSIN_EIS; 1.
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Marapsin precursor (EC 3.4.21.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 AA;
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Q28661;
                                                                                                                                                                              proteinase.
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ACT_SITE
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CARBOHYD
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REQUIRED FOR SPECIFICITY (BY SIMILARITY).

Aleobciellaada468 CRC64;
                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                               TRYPSIN ZETA.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
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SIMILARITY)
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InterPro; IPR001254; Ser_protease_Try.
Frem; PF000189; trypsin; 1.
PRINTS; PR0072; CHYMOTRYSIN.
SMART; SM0020; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Multigene family.
SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.6%; Score 70; DB 1; 70.0%; Pred. No. 0.012; tive 1; Mismatches
                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin zeta precursor (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                    281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0015083; Dere\Try-zeta.
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29735 MW;
                                                                                                                                                                                       Drosophila erecta (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U40653; AAA83236.1; -. HSSP; P00763; 1DPO.
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                                                                STANDARD;
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281 AA;
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.112;
                                                                                                                                                                                                                                                               NCBI_TaxID-7220,
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16-OCT-2001 (
15-JUN-2002 (
                                                                  TRYZ DROER
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MPN_HUMAN
ID MPN_HUMAN
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CHAIN
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                                                                                   P54630;
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ð 셤 **42444**

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51087 MW;
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                                22
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            MOD_RES
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KLKF_HUMAN
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                                                                                            AND VILIA.
SURDNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOWDULLIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood coagulation; Glycoprotein; Serine protease; Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal. NON_TER
                            TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
PTM: THE VITAMIN R-DEPENDENT, ENZIMATIC CARBOXILATION OF SOME
GEU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
MISCELLANBOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFIXITY TO
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
SITE IS NECESSARY FOR THE RECCGNITION OF THE
THROMBIN-THROMBOMODULIN COMPLEX.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PROTEIN K-DEPENDENT PROTEIN C.
PROTEIN C HIGHT CHAIN (BY SIMILARITY).
PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROWBIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000152; Asx_hydroxyl.
Interpro; IPR001561; BGF-like.
Interpro; IPR001881; BGF_Ca.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR000294; Vitk_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF_2; 2.
EGF_CA; 1.
EGL_CARBOXYLATION; 1
TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00134; TRYPSIN_HIS; 1. PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                 EMBL; U49933; AAA92956.1; -. HSSP; P04070; 1PCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00181; EGF;
SMART; SM00069; GLA;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSITE; PS50240;
                       'ISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
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Gaps
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SEQUENCE FROM N.A.
SEQUENCE 20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
Moss P., Paeper B., Wang K.;
"Taging of the serine protease gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-11010966;
Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
Wholecular cloning of the human kallikrein 15 gene (KLK15). Upregulation in prostate cancer.";
J. Biol. Chem. 276:53-61(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY)
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 458,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                ĠAMMA-CARBOXYĞLÜTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYĞLÜTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                        GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                        GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                         GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D75A5F990C8F29D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OGHARS, OGHARG, OGHARG, OGHARG, QGHARG, 16-OCT-2001 (Page 14 OCT-201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 1;
Pred. No. 0.038;
                                                                                                                                                                (BY SIMILARITY).
                                                                                                                                                                                                                                                      BY SIMILARITY).
                                                                     BY SIMILARITY)
                                                                                                                  BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Serine protease; Transmembrane; Signal-anchor.

CHAIN 162 416 CATALYTIC CHAIN (POTENTIAL).

CHAIN 162 416 CATALYTIC CHAIN (POTENTIAL).

CTATALYTIC CHAIN (POTENTIAL).

CTYOPLASMIC (POTENTIAL).

TRANSMEM 17 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).
                                                                                                                                                                                                                                                                     protease, hepsin, from mouse preimplantation embryos.";
J. Biol. Chem. 272:31315-31320(1997).
                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                     MEDIINE-98058912; PubMed-9395459; Vu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.; "Identification and cloning of the membrane-associated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 1; Length 416;
Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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432194FF4004F848 CRC64;
                                                                                                                                                                                                                                                                                                                                                        |- SUBCELLULAR LOCATION: Type II membrane protein.
|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 AA
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SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MENONS; SOLIZZA, MENONS; SOLIZZA, MENONS; MEJ.1196620; HDD.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR0011254; Ser_receptor.
InterPro; IPR001190; Src_receptor.
Pfam: PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN,
SMART; SM00202; TRYPSIN,
PROSITE; PS50240; TRYPSIN, DOM; 1.
PROSITE; PS00134; TRYPSIN, DOM; 1.
PROSITE; PS00134; TRYPSIN, DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 GNQIKPKMFCAGYPEGGIDACQGDSGGPFV 357
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         Serine protease hepsin (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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ID HEPS_HUMAN STANDARD; I
AC P05981;
DT 01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF030065; AAB84221.1; -.
                                                                         Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44739 MW;
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                                                                                                                                                                                                                                                                                                                                          OF CELL MORPHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111
416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00763; 1DPO.
                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
DISULFID
DISULFID
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CARBOHYD
SEQUENCE
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY),
CHARGE RELAY SYSTEM (BY SIMILARITY),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISOFORM 3),
SHNEPGTAGSPRSQ -> PLSSP (IN REF. 2),
B5EBF8D6022786B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEGMIS, PEGO089; LIYPSAIN; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; TrYP_SPS. 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00144; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
MISSING (IN ISOFORM 4)
MISSING (IN ISOFORM 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 1;
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long amodified and this statement is not removed.
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[3]
PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X75363; CAA53145.1; ALT_SEQ
                                                                  MEDLINE-94289486; PubMed-8018728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF242195; AAG09469.1; -. EMBL; AF242195; AAG09470.1; -.
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EGRGAESCEGDSGGPLV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF242195; AAG09471.1
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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147
256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .081
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15-JUL-1998
15-JUL-1998
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEPS_MOUSE
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CONFLICT
SEQUENCE
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HEPS_MOUSE
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Gaps

9;

198

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ACT_SITE
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DISULFID
DISULFID
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                                                                DISULFID
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                                                                                                                                        Best Local
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     SHEFFFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease; Transmembrane; Signal-anchor.

1 162
NON-CAPALYTIC CHAIN (POTENTIAL).
163
417
CATALYTIC CHAIN (POTENTIAL).
1 17
CYTOPLASMIC (POTENTIAL).
18
44
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine
                                                                                                                                                                                                                                                                                                                                                                        mammalian cell growth.";
Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187(1993).
-1- FUNCTION: PLAYS AN ESSENTIAL ROLE IN CELL GROWTH AND MAINTENANCE
OF CELL MORPHOLOGY.
                                                                                                                                                           Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.; "A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain expressed by human liver and hepatoma cells.";
                                                                                                                                                                                                                                                                                                                                   MEDLINE-93348237; PubMed-8346233;
Torres-Rosado A., O'Shea K.S., Tsuji A., Chou S.H., Kurachi K.;
"Hepsin, a putative cell-surface serine protease, is required for
                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: PRESENT IN MOST TISSUES, WITH THE HIGHEST
LEVEL IN LIVER.
                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                   MEDLINE-91358502; Pubmed-1885621;
Tsuji A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S.,
Chou S.H., Kurachi K.;
                                                                                                                                                                                                                                                                         "Hepsin, a cell membrane-associated protease. Characterization, tissue distribution, and gene localization."; J. Biol. Chem. 266:16948-16953(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Ser_receptor.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00202; SR; 1.
SMART; SM00202; SR; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_LIS; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
                                                                                                                                    TISSUE=Liver;
MEDLINE=88209431; PubMed=2835076;
                                                                                                                                                                                                 Blochemistry 27:1067-1074(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M18930; AAA36013.1; -. EMBL; X07732; CAA30558.1; -. EMBL; X07002; CAA30058.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S00845; S00845.
HSSP; P00763; IDPO.
MEROPS; S01.224; -.
Genew; HGNC:5155; HPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
                                                               sapiens (Human).
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
                                                  TMPRS51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                  O.R
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Banganan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Andreise T., Trankhelm M., Attix C., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Glsen A.S., Carrano A.V.;

"Sequence analysis of chromosome 19q13.4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20229789; PubMed-10766816;
Yousef G.M., Chang A., Diamandis E.P.;
"Identification and characterization of KLK-L4, a new kallikrein-like
gene that appears to be down-regulated in breast cancer tissues.";
J. Biol. Chem. 275:11891-11898(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLIGIAR LOCARION: Secreted (Probable).
--- TISSUE SPECIFITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND SALIVARY GLAND.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLK13 OR KLKL4.
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                            .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                                                                                Length 417;
                                                                           INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POFI
                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                   B2086FF661E551D7 CRC64;
                                                                                                                                                                                                                                                                             DB 1;
0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 AA
                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                             Score 67;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                        329 GNQIKPKMFCAGYPEGGIDACQGDSGGFFV 358
                                                                                                                                                                                                                                                                                                                                                                                           2 GTRYKPDEGKRG-----DACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMEL; Ar135024; AAD26425.2; --
EMEL; AC011473; AAG23259.1; --
EMEL; AL050220; CAB43320.1; ALT_INIT.
                                                                                                                                                                                                                         45011 MW;
                                                                                                                                                                                                                                                                          47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-180 FROM N.A.
                                                                                                                                                                                                                                                                                                                                 15; Conservative
203
257
277
204
338
112
                                                                                                                                                                                                                   417 AA;
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
203
2257
3353
349
349
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                                                                                                                                                            DISULFID
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                 Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                            Score 65; DB 1; Length 157; Pred. No. 0.035;
                                                                                                                                                                                                                                                                               E8B1BACF49220DFB CRC64;
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                             MEROPS; SO1.218; ...
InterPoro; IRROO01254; Ser_protease_Try.
Pfam; PF00008; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS500134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_HIS; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 12, 2003, 15:36:42
Job time : 15.5 secs
                                                                                                                                                                                                                                                                               17262 MW;
                                                                                                                                                                                                                                                                                                            46.18;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                  115 GDSRDACEGDSGGPMV 130
                   EMBL; D43751; BAA07808.1;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                  10 GKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                               157
157 AA;
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SEQUENCE
                                                                                                                                                                                        ACT_SITE
DISULFID
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                                                                                                                                                                            ACT_SITE
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                                                                                                                                                                NON_TER
      à
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                                                                                                                                                                                                             CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCARC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID-9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                        46.5%; Score 65.5; DB 1; Length 277; 60.0%; Pred. No. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                              BA8A9E8DCFB5D542 CRC64;
                                                                                                             SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 AA.
                                                                                                                                                                                                      KALLIKREIN 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0010254; Ser_protease_Try.
Pfam. PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AGTK----EGGK-DSCEGDSGGFLV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGTRYKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                                                                                                                                                            30570 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 60.0
Matches 15; Conservative
          MEROPS; S01.306; -.
Genew; HGNC:6361; KLK13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                             170
277 AA;
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                                           MIM; 605505;
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Q28278;
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ACT_SITE
ACT_SITE
DISULFID
DISULFID
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Gaps

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4; Indels

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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088947 mus musculu 063207 rattus norv 060546 mesocricetu 090b10 mus musculu 09ws12 bombyx mori 09ws22 drosophila 08wxb4 homo sapien 076520 stomoxys ca 09xy5 ctenocephal 027083 tachypleus P79953 xenopus lae 09vxx5 drosophila 09vx5 drosophila
                       Q9cw97 mus musculu O18783 macropus eu O91674 xenopus lae Q9v5x8 drosophila Q8sq33 sus scrofa G63109 rattus norv Q9ttr0 canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   028511 macaca mula
09xy59 ctenocephal
09nbc9 glossina mo
09v1f5 drosophila
045029 drosophila
                                                                                                                                                                                                                             O54740 mus musculu
Q99132 mus musculu
Q9w5u8 drosophila
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"Fartial characterization of vertebrate prothrombin cDNAs:
Maplification and sequence analysis of the B chain of thrombin from nine different species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYPSIN FAMILY.
EMEL; MG1396; AAA31477.1; -.
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001234; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS0020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_I.
Hydrolase; Serine protease.
NON_TER
SEQUENCE 235 AA; 27093 MW; 92FF354F93F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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09XX55
027083
P79953
09VRX5
09BK47
                                                                                                                                     Q8SQ23
Q63109
Q9TTR0
                                                                                                                                                                                                                             054740
099L32
088947
                                                                                                                                                                                                                                                                                                             Q63207
Q60546
Q9DBI0
                                                                               Q91674
Q9V5X8
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08WZB4
076520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MD-2002 (TrEMBLrel. 20, MD-20-2)
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1004
2616
267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.217;
                                                                                  IISSUE-LIVER
                                                     \begin{array}{c} \lambda_0 \lambda_0 \\ 4 \lambda_4 \\ \lambda_0 \lambda_0 \\ \lambda_1 \lambda_1 \\ \lambda_2 \\ \lambda_3 \\ \lambda_4 \\ \lambda_4 \\ \lambda_1 \\ \lambda_1 \\ \lambda_2 \\ \lambda_3 \\ \lambda_4 \\ \lambda_5 \\ \lambda_5
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Q28731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990387 cynops pyrr
991004 gecko gecko
991001 gallus gall
991218 oncorhynchu
990504 eptatretus
990510 eptatretus
990510 drosophila
990wal drosophila
990wal drosophila
990wal buro japoni
990wal buro japoni
990wal buro japoni
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                                                                                                                                                                                             May 12, 2003, 15:32:37; Search time 56.5 Seconds (without alignments) 91.171 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671580
                          GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                       US-09-909-348-5
141
1 AGTRYKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
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Q91004
Q91001
Q9PTW7
Q91218
Q90504
Q90504
Q90WD2
Q90WD2
Q90WD8
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Q96RQ0
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
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sp_bacteriap:*
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sp_phage:*
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1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
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sp_human:*
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76.6
73.0
73.0
70.2
67.4
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29.6
6.6
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6.6
6.6
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6.6
6.6
7
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92FF3E4F93B360E0 CRC64;

Q9va44 drosophila Q96rq0 homo sapien

Score

Result õ 1117 108 103 103 103 103 70 70 70 70 69 68 68 68 67 5

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PubMed=1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Banfield D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                    MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               091001
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Q91001
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                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Cynops pyrrhogaster (Japanese common newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea; Salamandridae, Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Banfield D.K., MacGillivray R.T.A.; "Partial characterization of vertebrate prothrombin cDNAs: Amplification and sequence analysis of the B chain of thrombin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 89:2778-2783(1992).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
NCBI_TaxID=36310;
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       Length 235;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 AA; 27272 MW; 49264DD29A57A41F CRC64;
                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
    Score 117; DB 6;
Pred, No. 1.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMO0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNRNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_fry.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92212913; PubMed-1557383;
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                                                                                                                    167 YKPEEGKRGDACEGDSGGPFV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                            25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 YRPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M81395; AAA49391.1; -. HSSP; P00734; 1UVS.
    83.0%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.68;
90.58;
                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                            5 YKPDEGKRGDACEGDSGGPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gecko gecko (Tokay gecko).
Eukaryota; Metazoa; Chorda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nine different species.";
Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.6
Best Local Similarity 90.5
Matches 19; Conservative
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                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WCBI_TaxID=8330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     091004;
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                                                                                                                                                                                                                                                       090387
                                                                                                                                                                                                          RESULT 2
Q90387
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Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.; "Brolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin."; J. Mol. Evol. 38:177-187(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombin from
Banfield D.K., MacGillivray R.T.A.; Partial characterization of vertebrate prothrombin cDNAs: Amplification and sequence analysis of the B chain of thrombin from
                                                                                          nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Banfield D.K., MacGillivray R.T., "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; M81391; AAA21619.1; -.
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 AA; 26933 MW; 122A5C09F6F2276A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.0%; Score 103; DB 13;
81.0%; Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607 AA
                                                                                                                                                                                                                                                                                                InterPro; 1971/, interPro; 198001254; Ser_protease_Try. InterPro; 1PR001254; Ser_protease_Try. Pfam; PF000189; trypsin; 1. SMRT; SM00020; Trypsin; 1. PR05TTE; PS0240; Tryps_SPC; 1. PR05TTE; PS00134; TRYPSIN_BDM; 1. PR05TTE; PS00135; TRYPSIN_BTS; UNKNOWN_1. PR05TTE; PS00135; TRYPSIN_BTS; UNKNOWN_1. PR05TTE; PS00135; TRYPSIN_BTS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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InterPro; IPR002383; GLA_blood.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92212913; PubMed-1557383;
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MEDLINE-94223694; PubMed-7513365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YRPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                            EMBL; M81392; AAA49309.1;
HSSP; P00734; 1B7X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banfield D.K., MacGillivray R.T.A.;
Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; M81389; AAA49433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncorrynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                           73.0%; Score 103; DB 13; Length 608; 81.0%; Pred. No. 5.9e-07; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
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81.0%; Pred. No. 8.7e-07;
ive 2; Mismatches 2; Indels
        PROSITE; PSO0011; GLU_CARBOXYLATION; 1.
PROSITE; PSO0021; KRINGLE_1; 2.
PROSITE; PSSO240; KRINGLE_2; 2.
PROSITE; PSSO240; TRYPSIN_DOM; 1.
PROSITE; PSO0134; TRYPSIN_HIS; UNKNOWN_1.
HYDROLASE; SCAINE PROTECASES; 1.
HYDROLASE; SCAINE PROTECASES; 1.
SEQUENCE 608 AA; 69392 MW; 11B974B9AEE54EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 239 AA; 27396 MW; FOF43F9A3205BF38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      090504 PRELIMINARY; PRT; 420 AA. 090504; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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InterPro; IPR001254; Ser_protease_Try.
Pran; Pr00089; trypsin; IPR00180; CHYMOTRYPSIN.
SWART; SW00020; TRYP_SPC; I.
PROSITE; PS50240; TRYPSIN_DOW; I.
PROSITE; PS50134; TRYPSIN_LHIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_LHIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_LHIS; UNKNOWN_I.
PHYDTOLASE; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LIVER;
MEDLINE-92212913; Pubmed-1557383;
                                                                                                                                                                                                                                                                                                                                                                         539 YSPEDSKRGDACEGDSGGPFV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 FKPEEQKTGDACEGDSGGPFV 186
                                                                                                                                                                                                                                                                                                                                                 5 YKPDEGKRGDACEGDSGGPFV 25
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Best Local Similarity 81.0°
Matches 17; Conservative
                                                                                                                                                                                                                                         Query Match 73.0
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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090504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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"Purlifaction and Characterization of Gettrion prothrombin.";
Int. J. Blochem. Cell Biol. 32:1151-1159(2000)
Int. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE EMBL; ABOL28871; BAA89046.1; -.
HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Struthio camelus (Ostrich).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 103; DB 13; Length 607;
Pred. No. 5.9e-07;
2; Mismatches 2; Indels (
R InterPro; IPR003966; Prothrombin.
R InterPro; IPR001254; Ser_protease_Try.
R Péan; PF00594; VitK_dep_GLA.
R Péan; PF00051; Kringle; 2.
R Péan; PF00089; trypsin; 1.
R PRINTS; PR00001; GLABLOOD.
R PRINTS; PR001095; KRINGLE.
R PROSITE; PS00011; GLU_CARBOXILATION; 1.
R SMART; SM00010; TryP_SPC; 1.
R PROSITE; PS00011; GLU_CARBOXILATION; 1.
R PROSITE; PS00013; TRYPSIN_DOM; 1.
R PROSITE; PS00013; TRYPSIN_DOM; 1.
R PROSITE; PS00134; TRYPSIN_DOM; 1.
R PROSITE; PS00134; TRYPSIN_DOM; 1.
R PROSITE; PS00134; TRYPSIN_ERR; 1.
Hydrolase; Setine protease.
D SEQUENCE 607 AA; 69110 MW; 002F3605EA36270F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; PR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR000294; Vitk_dep_GlA.
Pfam; PF00544; gla; 1.
Pfam; PF00551; Kringle; 2.
Pfam; PF00099; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20579470; PubMed-11137455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 YSPEDSKRGDACEGDSGGPFV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.0%; 8
81.0%; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YKPDEGKRGDACEGDSGGPFV 25
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SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 81.0 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-8801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prothrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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Bayne C.J., Gerwick L., Fujlki K., Nakao M., Yano T.;
"Immune-relevant (including acute phase) genes identified in the
livers of rainbow trout, Oncorhynchus mykiss, by means of suppression
subtractive hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from
nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992),
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                        Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AF201359; AAG30034.1; --
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acipenser transmontanus (White sturgeon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Chondrostei, Acipenseriformes, Acipenseridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 88; DB 13; Length 172;
Pred. No. 2.6e-05;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 AA; 19873 MW; EC741FBA6957A887 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26846 MW; 45C558D6618E0585 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                          InterPro; INTERPOLISIA; Chymotrypsin.
InterPro; IPR001314; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMARI; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
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PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    minterpro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00022; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 FKPEEQKTGDAYEGDSGGPFV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.4%;
Best Local Similarity 76.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M81399; AAA48514.1; -. HSSP; P00734; 2HNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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NCBI_TaxID=7904;
                                                                                                                                                                                                                                                                                                                           MEROPS; S01.217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.; "Evolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin."; Mol. Evol. 38:177-187(194).
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                                                                                                                                                                                                                                                                                Banffeld D.K., MacGillivray R.T.;
"Partial characterization of vertebrate prothrombin cDNAs:
amplification and sequence analysis of the B chain of thrombin from
nine different species."
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
                                                       Eptatretus stoutii (Pacific hagfish).
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banfield D.K.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 420;
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Pred. No. 6.2e-06;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protesse:
SEQUENCE 420 As; 47888 MW; 64522AA21A57B67A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Thrombin B chain variant 1 (Fragment).
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                              MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94223694; PubMed-7513365;
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00722; CHYMOTRYPSIN,
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M81393; AAA21620.1; -. HSSP; P00734; IUVS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00051; kringle; 1
Pfam; PF00089; trypsin; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRYPSIN FAMILY
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                   NCBI_TaxID=7765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q9DFD1
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Gaps

us-09-909-348-5.rspt

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Ra dodson K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Ba dodson K. Joup L.B., Davmes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferracra S., Fleischmann W.,
RA Gong F., Gorgel J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Garder K., Gong F., Gorgel J.H., Gu Z., Gann P., Harris M.,
Ratris N.L., Harvey D., Helman T.J., Well M. H., Ibegwam C.,
RA Jalai M., Ralush F., Karpen G.H., Well M. H., Ibegwam C.,
RA Jalai M., Ralush F., Karpen G.H., Well M. H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lia Z.,
RA Mimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Martei B. M. Mortosh T.C., McLeod M.P., McDherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
RA Melson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler B.C., Stden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun R.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
Rh Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Rh Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RTYFSIN RAILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-OVIDDCTAL PARS RECTA;
Hiyoshi M., Takamune K., Mita K., Kubo H., Sugimoto Y., Katagiri C.;
"Oviductin, the oviductal protesse that mediates gamete interaction by
affecting the vitelline envelope in Bufo japonicus: Its molecular
cloning and analyses of expression and post-translational
activation.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buío japonicus (Japanese toad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Bufonidae, Bufo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70; DB 5; Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72151 MW; EFBDE951C8247949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flybase; FBgn0030925; CG6361.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00020; Tryp_SPc; 1.
SMSSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_ESE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRYPSIN FAMILY.
EMBL; AE003509; AAF48845.1; -.
HSSP; P20231; 1AAO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 DEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 61.1 les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-8387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oviductin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090WD8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y. H.C., Blazel R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxman B.P., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
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2., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawpe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Pred. No. 0.028;
4; Mismatches 3; Indels
                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY075342; AAL68205.1; -. SEQUENCE 378 AA; 40548 MW; D355D27E0E929ACC CRC64;
                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
     61.9%; Pred. No. 0.00028;
tive 4; Mismatches 4
                                                                                                                                                                                                                                                               378 AA
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NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                            PRT;
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                                                                                                           5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.18;
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Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 49.6
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                        GH17483p.
                                                                                                                                                                                                                                                         Q8SY50
Q8SY50;
                                                                                                                                                                                                                                                                                                                                                                                                                   CG6361
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09VWU2
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Gaps ö

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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                            Nakao M., Obsaka K., Kato Y., Fujiki K., Yano T.;
"Molecular cloning of complement Clr/Cls/MASP2-like serine proteases
from the common carp (Cyprinus carpio).";
Immunogenetics 52:255-263(2001).
--- SIMILARITY: CONTAINS 2 COB DOMAINS.
--- SIMILARITY: BECOUGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.K., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO1186; EGF_2; 1.
PROSITE; PSO1187; EGF_CA; UNKNOWN.1.
PROSITE; PSO0135; TRYPSIN.DOM; 1.
PROSITE; PSO0135; TRYPSIN.SER; 1.
SGF-11ke domain; Glycoprotein; Hydrolase; Hydroxylation; Setine protease.
SEQUENCE 686 AA: 76200 ...
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
031313 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000436; Sush1_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                     Chymotrypsin.
CUB_domain.
EGF-like.
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                                    PubMed-11220628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00181; EGF; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00020; TYP_ESPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                                                             Asx_hydroxyl
                                                                                                                                                                                                                                                             EMBL; AB042609; BAB17845.1; -. HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001881; EGF_Ca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00431; CUB; 2
Pfam; PF00008; EGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; sushi;
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                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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Matches
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         SOW WENT THE PROPERTY OF THE P
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"Mus muscullas mRNA for scrine protease-like gene spliced variant-1.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047758; BAB63919.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyprinus carplo (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         092406;
092406;
01-DEC-2001 (TERBLE1.19, Last sequence update)
01-DEC-2001 (TERBLE1.19, Last annotation update)
01-JUN-2002 (TERBLE1.21, Last annotation update)
Serine protease-like 1.
Mus musculus (Mouse)
Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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                                                                                                                                                                                                                                                                                                                                                                                   Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 11; Length 200;
Pred. No. 0.02;
                                                                                                Pfam; PF00431; CUB; 2.—
Pfam; PF00431; CUB; 2.
Pfam; PF000431; CUB; 2.
PROSITE: PS01180; CUB; 2.
PROSITE; PS01134; TRYPSIN_LOM; 2.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
HYdrolase; Serine protease.
SEOUENCE 974 AA; 107647 MW; F19705A470465553 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
PHYDROLASE; Protease.
SEQUENCE 200 AA; 22135 MW; 972959E4686EF603 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Score 70; DB 13
Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                           49.6%; Scor.
68.4%; Pred. No. v...
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                686 AA
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                                                InterPro; IPR000859; CUB_domain.
InterPro; IPR001254; Ser_protease_Try.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
EMBL; AB070367; BAB63372.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 PDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01,106;
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RESULT 13
092406
10 092400
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DT 01-DE
DT 01-DE
DT 01-DE
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Matches

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RESULT 14 Q9DGC2

Matches

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke E., Canter A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke E., Canter A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke E., Davies P.,
RA Cherry J.M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
BA Durbin K.J. Evangelista C.C., Ferraz C., Ferricas S., Fleischmann W.,
RA Durbin K.J. Evangelista C.C., Ferraz C., Ferricas S., Fleischmann W.,
R. Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Alali M., Ralush F., Karpen G.H., Re Z., Keinlson J.A., Ketchum K.A.,
Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lai J.M., Malush F., Karpen G.H., Re Z., Keinlson D.,
Ra Lasko P., Lei Y. Lei Y. Karft C., Kravitz S., Kulp D., Lai Z.,
Lu X., Mattei B., McIntosh T.C., McLeod M.P., Mopherson D.,
Rattei B., McIntosh T.C., McLeod M.P., Mopherson D.,
Ratkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Ralush K., Nelson K.A., Nixon K., Nisskern D.R., Pacleb J.M.,
Ralush K., Nelson K.A., Nixon K., Nisskern D.R., Pacleb J.M.,
Ralush W., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G.,
Ranert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
Rang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rang X.H., Rood F.N., Zhong W., Zhon X., Zhu X., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40937 MW; E1E54E03F2CDE2AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR001314; Chymotrypsin.
nterPro; IPR001254; Ser_protease_Try.
fam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003775; AAF57079.1; -. HSSP; P00763; 1DPO.
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Score 67.5; DB 5; Length 370; Pred. No. 0.065; Indels Mismatches Query Match Best Local Similarity 66.74 Matches 12; Conservative ò

309 EGRSRGDSCDGDSGGPLM 326 9 EGK-RGDACEGDSGGPFV 25 a

Search completed: May 12, 2003, 15:38:46 Job time: 57.5 secs

Scoring table: Perfect score: Sequence:

Searched:

Minimum DB Maximum DB

Database

OM protein

Run on:

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Novel tripoptide i
Calpain inhibitor.
ACE inhibitor pept
IGF-1 analogue N-t
Angiotensin conver
ACE inhibiting tri
Microbial emetic t
Apolipoprotein A-I
Apolipoprotein A-I
Apolipoprotein A-I
Non RGD, non-YISGR
Potential cross-11
                                                                         Cathepsin G inhibi
HIV protease inhib
Novel tripeptide i
                                                                                                                                                                                                                                                                                                        LDV-peptide capabl
VTL-peptide capabl
Peptide for diagno
                               Chromophore-contg.
Elastase inhibitor
Elastase inhibitor
                                                                                                                                                                                                                                                                                                                                                                  Angiotensin II pep
Peptide AII(1-3) u
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal-transducing
                                                                                                                                                                                                                                                                                       Beta-amyloid modul
                                                                                                                                                                                                                                                                                                                                                                                              Anti-inflammatory
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                                                                                                                                                                                                                                                                                                                                                    Murine signalling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New ERA binding domain polypeptides and polynucleotides encoding them, useful as research reagents and materials for discovery of treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERA binding domain; Escherichia coli; GTPase; antimicrobial; antibacterial; antiblotic; pathogenesis; infection; vaccine; peptide therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERA binding domain polypeptide SEQ ID NO 159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                             AAR38408
AAR38409
                                                                                                                                                                   AAR58565
                                                                            AAR38411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2001; 2001WO-US01786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2000; 2000US-0176870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476108/51.
WO200153458-A2
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Hypotensive oligop
Elastase-inhibitin
Cathepsin G inhibi
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ERA binding domain
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New antihypertensi
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                                                                                               May 12, 2003, 15:31:22 ; Search time 2.86 Seconds (without alignments) 46:591 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                | SIDS/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1986.DAT:*
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/SIDS2/gcgdata/geneseq/genesegp-embl/AA2001.
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                                                                                                                                                                                                                                                                                                  908470
              GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
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                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        using sw model
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AAP90664
AAP90665
AAP90678
AAR10543
AAR29095
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
                                                                                                                                                              US-09-909-348-4
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    protein search,

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Match Length
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Pred. No.

Score

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Result

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                      AAB91888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to ERA binding domain polypeptides ARG99559-AAG999989 and AAW00010-AAW00021). The era gene in Escherichia coli codes for an essential GFPase protein able to autophosphorylate at serine and/or threonine residues. The protein has potential antimicrobial and antibacterial activity and is useful in screening for antagonists, agonists and for compounds with antibiotic activity. The proteins are also useful in determining their role in pathogenesis of infection, dysfunction and disease and could be used as part of a vaccine and/or
                                                                              (AAG95559-AAG99999 and AAM00010-AAM00021). The era gene in Escherichia coli codes for an essential Grease protein able to autophosphorylate at serine and/or incenine residues. The protein has potential antimicrobial and antibacterial activity and is useful in screening for antagonists, agonists and for compounds with antibiotic activity. The proteins are also useful in determining their role in pathogenesis of infection, dysfunction and disease and could be used as part of a vaccine and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New ERA binding domain polypeptides and polynucleotides encoding them, useful as research reagents and materials for discovery of treatments and diagnostics for diseases, or for genetic immunisation -
                                                                                                                                                                                                                                                                                                      Gaps
                                                                   The present invention relates to ERA binding domain polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERA binding domain; Escherichia coli; GTPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; antiblotic; pathogenesis; infection; vaccine;
and diagnostics for diseases, or for genetic immunisation
                                                                                                                                                                                                                                                                      Length 2;
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                                                                                                                                                                                                                                                                    Score 4; DB 22; L Pred. No. 7.2e+05; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERA binding domain polypeptide SEQ ID NO 183.
                                Claim 1; Page 26; 279pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG99741 standard; Peptide; 2 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 29; 279pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lupas AN, Pearce KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-476108/51.
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                   2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AA;
                                                                                                                                                                                                    peptide therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      maleimido group; amino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino, hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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   Length 2;
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   DB 22; L
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100.0%; Pred. No. 7.2e+05;
tive 0; Mismatches 0;
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                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis related peptide SEQ ID NO:1064
      Score 4;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                AAB91888 standard; Peptide; 2 AA.
100.0%; Sillarity 100.0%; P. Conservative 0;
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                     capsules, granules, powder, syrup, suspension, suppositories, ointment, cream, gel, plaster, inhalation compsn. or injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                    The peptide and its salts inhibit angiotensin-converting enzyme (ACE) and are useful as antihypertensives. They may be administered orally, parenterally or rectally in the form of tablets,
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100.0%; Pred. No. 7.2e+05;
ive 0; Mismatches 0;
                                                                                                            New antihypertensive peptide(s) - used to inhibit angiotensin-converting enzyme
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                           (AJIN ) AJINOMOTO KK.
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Best Local Similarity
Matches 1; Conserv
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7.2e+05;
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                                                                                                                                                                                                    Peptides may be derived from extract of fig, and are hypotensive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cathepsin G; elastase; connective tissue; degradation; protease; gout; rheumatoid arthritis; emphysema; ARDS; adult respiratory distress syndrome; para-phenylene.
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by
                                                                                               New oligopeptide hypotensive drug - based on alanine, valine, asparagine, proline, isoleucine and arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.e.
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                                                                                                                                                                                                                                                                                                      Length 3;
                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mehd1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -C(0)-para-phenylene-C(0)-"
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                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 4; DB 12; L. Best Local Similarity 100.0%; Pred. No. 7.2e+05; Matches 1; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR29095 standard; peptide; 3 AA.
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                                                                                                                                                            Claim 1; Page 843; 9pp; Japanese.
(AGEN ) AGENCY OF IND SCI TECH. (SHOS ) SHOWA SANGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RICH ) MERRELL DOW PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elastase-inhibiting fragment.
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/note=
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                                                          WPI; 1991-004480/01.
                                                                                                                                                                                                                                                              3 AA;
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Peet NP;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The peptide and its salts inhibit angiotensin-converting enzyme (ACE) and are useful as antihypertensives. They may be administered orally, parenterally or rectally in the form of tablets, capsules, granules, powder, syrup, suspension, suppositories, olintment, cream, gel, plaster, inhalation compsn. or injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
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                                                                                                                                                                                                                                                          Antihypertensive peptide; angiotensin-converting enzyme;
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100.0%; Score 4; DB 10; I
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 1; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antihypertensive peptide(s) - used to inhibit angiotensin-converting enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR10543 standard; Protein; 3 AA.
                                                                                               AAP90678 standard; protein; 3 AA
                                                                                                                                                                                                                    New antihypertensive peptide
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                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AJIN ) AJINOMOTO KK
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Sequence

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AAR10543 RESULT

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WPI; 1993-021449/03.
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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                3 AA;
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Modified-site
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AAR34023
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The N-terminal amino acids of the peptides of AAR29095-96 are linked by -C(0) paraphenylene-C(0). The cpd has an anti-inflammatory effect useful in the treatment of gout, rheumatoid arthritis and other inflammatory diseases and to prevent elastin mediated issue damage. It can also be used in the treatment of emphysema and adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linked by -C(0) paraphenylene-C(0).
The cpd. has an anti-inflammatory effect useful in the treatment of gout, rheumatoid arthritis and other inflammatory diseases and to prevent elastin mediated tissue damage. It can also be used in the treatment of emphysema and adult respiratory distress syndrome.
                                                                                                                              Gaps
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The N-terminal amino acids of the peptides of AAR29095-96 are
                                                                                                                                                                                                                                                                                                                           Cathepsin G; elastase; connective tissue; degradation; protease; gout; rheumatoid arthritis; emphysema; ARDS; adult respiratory distress syndrome; para-phenylene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide derivs. used as cathepsin G and elastase inhibitors for treating gout, rheumatoid arthritis, inflammatory disorders, emphysema and adult respiratory distress syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                         the peptides
                                                                                                     100.0%; Score 4; DB 13; Length 3; 100.0%; Pred. No. 7.2e+05; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                 AAR29096 standard; peptide; 3 AA.
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                                                                                                                                                                                                                                                                                                     Cathepsin G inhibiting fragment.
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                                                                                                                             1; Conservative
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                                                                                                                Local Similarity
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Modified-site
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                                                                               Sequence
                                                                                                                                                                                                                                                       AAR29096;
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AAR29096
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   Length 3;
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DB 13; I
7.2e+05;
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100.0%; Pred. No. 7.2e+05;
ive 0; Mismatches 0;
Score 4; DB ]
Pred. No. 7.26
); Mismatches
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                                                                                                                                                                                                                                                                                                        Metal trapping peptide intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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100.0%; Sc
100.0%; Pr
iive 0;
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                                   Conservative
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/label= N6-(2-carboxybenzoyl)lysine
/note= "Linked via a linking chain such as
-CO-phenylene-CO- to the N-terminal of a
cathepsin G inhibiting molecule as described
in AAR38410-11"
                                                                                                                                                                                                                                                                                                                                                                 The opd. is used for determining interleukin-lbeta convertase (ICE) activity. ICE has been implicated in inflammatory and immune-based diseases including diseases of the lungs and airways, CNS, eyes, ears, joints, bones and connective tissues, cardiovascular system (including the pericardium), GI and urogenital systems and skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "May opt. be modified by COCOR, CF2CF3, CF3, CHF2, COOR3, CONHR3, CF2CHR3CONHR, H, alkyl, arXiv, aralkyl or COR; where R3 is H, alkyl, aphenyl or benzyl and R is OH or alkoxy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammatory disease; prevention; rheumatoid arthritis; emphysema; neutrophil-mediated connective tissue degradation; gout; elastase; inhibition; adult respiratory distress syndrome.
                                                                                                                                                                                            Maccoss M, Mumford RA, Thornberry NA;
                                                                                                                                                                                                                                                                        New chromophore-contg. cpds. for determining interleukin-lbeta convertase activity in diagnosis of inflammatory or immune-based
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100.0%; Pred. No. 7.2e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elastase inhibitor peptide #2.
                                                                                                             910S-0746455.
                                                                                 92EP-0202450
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                                                                                                                                                                                              Hagmann WK,
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                                                                                                                                                              (MERI ) MERCK & CO INC
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mucosal membranes
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Modified-site
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                                                                                 08-AUG-1992;
                                                                                                             16-AUG-1991;
17-DEC-1991;
                                                                                                                                                                                          Chapman KT,
Weldner JR;
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                   EP528487-A.
                                                 24-FEB-1993
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                                                                                                                                                                                                                                                                                                       disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The acyclic peptide (see AAR31340) with metal trapping activity may produced by fragment condensation using the peptide fragments given AAR34022-29
                                                                                                                                                                                                                                     "Cys(Acm); Acm- acetamidomethyl-protected SH of cysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "alaninyl 7-amino-4-methylcoumarin amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New acyclic peptide with metal trapping activity - exhibits in vivo metal transporting action and can be used as drug, diagnostic agent or functional material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromophore-contg. cpd. for determining ICE activity (3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                            Electrostatic interaction; metalloprotein; binding site; protecting group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-1beta; IL-1b; inflammation; immune; disease; diagnosis; 7-amino-4-methylcoumarin amide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 4; DB 14; Ilarity 100.0%; Pred. No. 7.2e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-acetyl-tyrosinyl"
                                                                                                                                                                                                                                                                                    /note- "OMe protected"
                                                              Metal trapping peptide intermediate
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                        'note= "HCl.H-Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                               X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR34623 standard; peptide; 3 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 2; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (ICHI-) ICHIKAWA GOSEI KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                 91JP-0120196,
                                                                                                                                                                                                                                                                                                                                                                                91JP-0120196
                               (first entry)
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                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-021449/03,
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Best Local Similarity
Matches 1; Conserv
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Modified-site
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                               19-MAY-1993
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                                                                                                                                                                                                                                                                                                                 JP04346999-A
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                                                                                                                                          Synthetic.
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AAR34023;
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AAR3462

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"Linked via a linking chain such as -CO-phenylene-CO- to the N-terminal of a Cathepsin G inhibiting molecule as described in AAR38410-11"
                                                                                                                                                                                                                                 sequences given in AAR38407-09 are elastase inhibiting peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    May opt. be modified by COCOR, CF2CF3, CF3, CHE2, COOR3, CONNAI, CF2CHR3CONHE, H, alkyl, arryl, aralkyl or COR; where R3 is H, alkyl, phenyl or benzyl and R is OH or alkoxy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammatory disease; prevention; rheumatoid arthritis; emphysema; neutrophil-mediated connective tissue degradation; gout; elastase; inhibition; adult respiratory distress syndrome.
                                                                                                                                                                                                                                                 which were produced by standard peptide synthesis methods. In the context of the invention they are linked via their N-termini to a Cathepsin G inhibiting peptide (see features table). The peptide conjugates may be used to prevent neutrophil-mediated connective
                                                                                                                                                                                                                                                                                                     tissue degradation associated with inflammatory diseases eg. gout and rheumatoid arthritis. They may also be used for preventing elastin-mediated tissue damage in the treatment of emphysema and
                                                                                                                                                              cathepsin G and elastase inhibitors - prevents connective
                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 3; 7.2e+05;
                                                                                               Janusz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 4; DB
100.0%; Pred. No. 7.2
:1ve 0; Mismatches
                                                                                             Doherty NS,
                                                                                                                                                                                                                                                                                                                                                adult respiratory distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                          Claim 9-12; Page 51; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR38409 standard; Protein; 3 AA
                                                                  (RICH ) MERRELL DOW PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elastase inhibitor peptide #3.
                                        91US-0704499
              92ZA-0003602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92ZA-0003602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 1; Conservative
                                                                                            Веу Р,
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/note=
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                                                                                                                                    WPI; 1993-197380/24
                                                                                                                                                                              tissue degradation
                                                                                                                                                                                                                                                                                                                                                                            3 AA;
                                                                                             Angelastro MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
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           18-MAY-1992;
                                     23-MAY-1991;
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Gaps

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Indels

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                    New cathepsin G and elastase inhibitors - prevents connective
                                             Mehd1 S;
                                                                                                                                                                                                                                                                                                                                                                                Length 3;
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                                                                                                                                                                                                                                                                                                                                                                               DB 14; L
7.2e+05;
                                           Doherty NS, Janusz MJ,
                                                                                                                                                                                                                                                                                                                                                                               Score 4; DB 1
Pred. No. 7.26
; Mismatches
                                                                                                                                                                                                                                                                                                                   adult respiratory distress syndrome.
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                                                                                                                                                               Claim 9-12; Page 51; 55pp; English
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                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
              (RICH ) MERRELL DOW PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                           Bey P,
                                                                                    WPI; 1993-197380/24
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                   tissue degradation
                                                                                                                                                                                                                                                                                                                                                 3 AA;
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                                        Angelastro MM,
Peet NP;
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Appl Appl

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Sequence
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Patent No. 5464821
GENERAL INFORMATION:
APPLICANT: ASSULT-OLISEN, Stig
APPLICANT: WIDMER, Fred
APPLICANT: GAURI, Kailash
TITLE OF INVENTION: Small peptidic compounds useful for the
TITLE OF INVENTION: treatment of Glaucoma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                          US-08-321-585A-1
US-08-37-392-5
US-08-634-06-36
US-08-53-11
US-07-955-905A-11
US-08-293-150A-38
US-08-408-604A-164
US-08-478-386A-40
US-08-408-858A-14
US-08-408-888A-14
US-08-408-888A-14
                                                                                                                                                                                                                     US-08-451-822A-18
US-08-388-653-40
                                                                                                                                                                                        US-08-408-858A-21
                                                                                                                                                                                                                                                   08-473-985-40
                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91 .
FILING DATE: 25-MAR:1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 25-MAR:1992
ATTOWNEY/AGENT INFORMATION:
NAME: IWANT. JOHN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 S. Wacker Dr.
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/122,510 FILING DATE: 24-SEP-1993 CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
REFERENCE/POCKET NUMBER: 93,8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,628
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FEATURE: NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                        US-08-122-510-9
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STATE:
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Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, App
Sequence 6, App
Sequence 139, 2
Sequence 3, App
                                                                                                // Search time 0.96 Seconds
(without alignments)
30.649 Million cell updates/sec
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Sequence 14,
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Sequence 30,
Sequence 5,
Sequence 5,
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Sequence 13,
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Sequence 8
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/RB_COMB.pep:*
/cgn2_6/ptodata/1/laa/RCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
             GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08 603-737-18

US-09-264-709A-29

US-09-264-709A-30

PCT-US94-10475-5

US-07-729-099-5

US-07-729-099-5

US-08-118-135A-8

US-07-947-035-3

US-08-384-618-1

US-08-384-618-1

US-08-122-510-7

US-08-122-510-7

US-08-122-510-8

US-08-122-510-8

US-08-122-510-11

US-08-122-510-11

US-08-122-510-11

US-08-122-510-11

US-08-122-510-11

US-08-122-510-11
                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
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-08-213-897A-9
                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                May 12, 2003, 15:33:37
                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
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Maximum DB s
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                                                                                                    Run on:
                                                                                                                                                         Title:
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CORRESPONDENCE ADDRESS:
STREET: 10 S. Wacker Dr.
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COURRENT APPLICATION DATA:

APPLICATION DATA:

CLASSIFICATION 105/08/122,510

FILING DATE: 24-SEP-1993

RIOR APPLICATION: 514
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US-08-122-510-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: IWanicki, John P
REFISTATION NUMBER: 34.628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
APPLICATION NUMBER: PCT/DK92/000
                                                                                                                                                                                                                                              Sequence 14, Application US/08122510
Patent No. 546481
GENERAL INFORMATION:
APPLICANT: AASMUL-OLSEN, Stig
APPLICANT: WIDMER, Fred
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US-08-127-904-5
; Sequence 5, Application US/08127904
; Beten No. 5470951
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                WIDMER, Fred
GAURI, Kailash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: AASMUL-OLSEN, Stig
APPLICANT: WIDMER, Fred
APPLICANT: GAUFI, Kailah
TITLE OF INVENTION: Small peptidic compounds useful for the
TITLE OF INVENTION: treatment of Glaucoma
WUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 4; DB 1; Length 2; Conservative 0; Mismatches
                                                                                                                                                                                          100.0%; Score 4; DB 1; Length 2; 100.0%; Pred. No. 1.7e+05;
...CCATION: 1..2
; OTHER INFORMATION: /note= "Where X is Benzylester;
; OTHER INFORMATION:
; OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,510
FILING DATE: 24-SEP-1993
CLASSIFICATION NUMBER: DK 0532/91
PRIOR APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
PRIOR APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
APPLICATION NUMBER: AS-MAR-1992
ATTONEX/AGENT INFORMATION:
ANDER AREA ASSAMATION:
ANDER ASSAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Where X is Benzylester
                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 S. Wacker Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08122510
Patent No. 5464821
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 9:
TELECOMMUNICATION INFORMATION
TELEPHONE: 312-715-1000
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TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1.2
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Sequence 29, Application US/09264709A
Patent No. 6320024
GENERAL INFORMATION
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
TITLE OF INVENTION: Improve the Quality of Life
TITLE OF INVENTION: Improve the Quality of Life
TITLE OF INVENTION: Improve the Quality of Life
CURRENT APPLICATION NUMBER: US/09/264,709A
CURRENT APPLICATION NUMBER: 08/79/782
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 4; DB 2; Length 2; 100.0%; Pred. No. 1.7e+05; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: memory-modulating peptide
US-09-264-709A-29
                                                                                                       39,911
R: 2026-4186
                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELESA: (212) 751-6849
TELES: 421792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                NAME: Elizabeth A. Bogosian
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                              FILING DATE: TTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                    C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Xaa
OTHER INFORMATION: pher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DESCRIPTION: peptide HYPOTHETICAL: NO
  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
Matches 1; Conserva
                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-264-709A-29
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Fatent No. 5849691
GENERAL INFORMATION:
FAPLICANT: Major: et al.
TITLE OF INVENTION: of Cathepsin D and Plasmepsins I and II
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNECAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                                                                                                                                          STATE: California
COUNTRY: United States of America
21P: 91010-0269
COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
COMPUTER: A September 1993
FILING DATE: 29 September 1993
CLASSTEICATION 1424
PRIOR APPLICATION DATA: NO. 5470951e
                                        Protein and Improving the
Quality of Life in Individuals
With Alzheimer Disease
                       Amnestic Effects of Amyloid n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7e+05;
  Method For Antagonizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:

NAME: Irons, Edward S.

REGISTRATION NUMBER: 16.541

REFERENCE/DOCKET NUMBER: No. 5470951e

TELECOMMUNICATION INFORMATION:

TELEPRAX: (202) 783-640

TELEPRAX: (202) 783-640

TELEPRAX: (202) 783-611

IRORMATION FOR SEQ ID NO: 5:
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FILING DATE: February 20, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDFERFECT 5.1 CURRENT APPLICATION DATA
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
MENTER: IBM PC COMPATIBLE
THERE FORMS PC-DOS/MS-D
                                                                                                                                     E: City of Hope
1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Best Lócal Similarity 100...
1, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Meth
TITLE OF INVENTION: Amne
TITLE OF INVENTION: Prot
TITLE OF INVENTION: Qual
TITLE OF INVENTION: WITH
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                CITY: Duarte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-127-904-5
                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 AURRENT APPLICATION DATA:
AUBLICATION NUMBER: US/07/729,099
FILING DATE: 19910712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                red. No. 1.7e+05;
Mismatches 0;
                                                                                                                                                                                                                                                        red. No. 1.7e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Binger, Mary-Helen
APPLICANT: Braamontes, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOffmann-La Roche Inc.
                526-3564 or 783-6030
                                                                                                                                                                                                                                 100.0%; Score 4;
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 4; Best Local Similarity 100.0%; Pred. No. Matches 1; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/07729099
Patent No. 5403581
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ROSEMAN, Catherine R
REGISTRATION NUMBER: 34,24(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 8
TELECOMMUNICATION INFORMATION
                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Elmeria tenella
                                 TELEX: None
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2
                  (202) 626-35
(202) 783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: YES
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                                                                                                                                   Amino Acid
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                     TYPE: Amino
STRANDEDNESS
                TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                          ; TOPOLOGY:
PCT-US94-10475-5
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                                                                                                                           APPLICANT: Roberts, Eugene
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
TITLE OF INVENTION: Improve the Quality of Life
FILE REPRENCE: 2124-310
CURRENT PELING DATE: 1999-03-09
PRIOR PEPLICATION NUMBER: 08/797,782
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin. Ver. 2.1
SEQ ID NO 30
LENGTH: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 4; DB 4; Length 2;
llarity 100.0%; Pred. No. 1.7e+05;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Description of Artificial Sequence: CTHER INFORMATION: memory-modulating peptide US-09-264-709A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antagonizing Amnestic
Effects of Amyloid n
Protein and Improving
the Quality of Life
in Individuals
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Serial No.
08/127,904; filled
29 September 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      With Alzheimer Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
COUNTRY: United States of America
ZIP: 91010-0269
COMPOTER. READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4"
MEDIUM TYPE: diskette
COMPOTER: Wang PC
COMPOTER: Wang PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS DOS Version 3.20
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FILING DATE: 16 September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application PC/TUS9410475 GENERAL INFORMATION:
                                                              Sequence 30, Application US/09264709A
Patent No. 6320024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: City of Hope
1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: NO
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: U. PRIOR APPLICATION DATA: SER PRIOR APPLICATION DATA: 08, PRIOR APPLICATION DATA: 29 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1; Conserv
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                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duarte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US94-10475-5
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APPLICANT: Walton, Paul E.
APPLICANT: Walton, Paul E.
APPLICANT: Ballard, Francis J.
APPLICANT: Manuty, John P.
TITLE OF INVENTION: Method of Administering IGF-1, IGF-2, TITLE OF INVENTION: and Analogs Thereof to Birds
NUMBER OF SEQUENCES: 18
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Mord 5.5-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/118,135A
FILING DATE: September 8, 1993
CLASSIRICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA: NO. 5437982e
ATTORNOR APPLICATION DATA: NO. 5437982e
ATTORNOR APPLICATION DATA: NO. 5437982e
ATTORNOR APPLICATION NUMBER: UFW16993
REFERENCE/DOCKET NUMBER: UFW16993
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAK: 1-206-682-8100; 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 anning acids
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APPLICATION NUMBER: US/07/947,035 FILING DATE: 17-SEP-1992 CLASSIFICATION: 514 CLASSIFICATION: 514 NUMBE: 51bley, Kenneth D. REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 4; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 1; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
DESCRIPTION: page 22, line 17; VFM
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COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Renneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5444045th Carolina
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/07947035 Patent No. 5444045
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 8R1-21-0
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(919) 881-3175
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INFORMATION FOR SEQ ID NO:
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Patent No. 5437982
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
OURRESOURCE ADDRESS:
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF TITLE OF INVENTION: TREATING USING THE SAME NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 4; DB 1; Length 3; 100.0%; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: BURNS.

AUDRESSEE: BURNS. Doane, Swecker & Mathis STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
Z1P: 22313-1404

COMPUTER REDABLE FORM:
MEDIOW TYPE: Rioppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
FILING DATE: 13-NOV-1991
FILING BAPLICATION: 435
PROGRAMMENTED PROGR
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REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                  Sequence 38, Application US/07791213D Patent No. 5409895
                                                                                                                                                                                                                         MORISHITA, Hideaki
KANAMORI, Toshinori
NOBUHARA, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 amino acids
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Best Local Similarity
Matches 1; Conserv
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GENERAL INFORMATION:
APPLICANT: Suzuki, Nacyoshi
TITLE OF INVENTION: A No. 5464819el Physiologically Active Peptide Having
TITLE OF INVENTION: Immunoregulatory Activities
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: United States of America
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BURTON, James
APPLICANT: BURTON, James
APPLICANT: DONG, Zhengxin
APPLICANT: FRIGO, Timothy B.
TITLE OF INVENTION: SPECIFIC INHIBITORS OF TISSUE KALLIKREIN
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 555 13th Street, N.W., Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 4; DB 1; Length 3; Best Local Similarity. 100.0%; Pred. No. 1.7e+05; Matches 1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/729,353
FILING DATE: 19910712
CLASSIFICATION: 514
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Patent No. 5464820
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-182714
FILING DATE: 12-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                             Sequence 6, Application US/07729353 Patent No. 5464819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,330 REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
TELEPHONE: 703 241 1300
TELEFAX: 703 532 3407
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-07-729-353-6
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CITY: Wa
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APPLICANT: Takano, Toshiaki
TITLE OF INVENTION: Angiotensin Convertin Enzyme Inhibitor
TITLE OF INVENTION: and Method for Preparing Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3;
                                                                                                                                                                                             Length 3;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 4; DB 1; Le
ilarity 100.0%; Pred. No. 1.7e+05;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                             Score 4;
Pred. No.
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FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ludwiig, S. Peter
RESISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 4703/08827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/090,530
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Patent No. 5449661
GENERAL INFORMATION:
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TELEPHONE: (212)527-7700
TELEFAX: (212)753-7513
                                                                                                                                                                                           100.0%;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS LENGTH: 3 amino acids
                                                                                                                                                                                                                                     Conservative
                                                                                                     : peptide
NO
                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1; Conserva
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                                                                                     linear
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
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                                                                                   TOPOLOGY: III
MOLECULE TYPE:
HYPOTHETICAL: I
US-07-947-035-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 10022
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US-08-384-618-1
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-384-618-1
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STATE: D.C.

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COMPUTEY: U. O. S. A.

ZIP: 20004-1109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PACONICALIDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PACENITIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,812
FILING DATE: 22-UN1-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rememblek, James
REGISTRATION NUMBER: 16865-0118
TELEPRAY: (202) 639-7832
INFORMATION POR: SEQ ID NO: 139:
SEQUENCE CIRRACTERISTICS:
LENGTH: 3 amino acids
TYPE amino acids
TYPE amino acids
STRANDEDRESS: single
MOLECULE TYPE: peptide
FRATURE:
NAME/KEY: Modified-site
LOCATION: 3
US-08-079-812-139
Query Match
Best Local Stailarity 100.0%; Pred: No: 1.76+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: May 12, 2003, 15:40:40 Job time : 1.96 secs

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Query Match
Best Local Similarity
Matches 1; Conserv
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Sequence 464, App
Sequence 11, App11
Sequence 5, App11
Sequence 6, App11
Sequence 63, App11
Sequence 71, App1
Sequence 71, App1
Sequence 11, App1
Sequence 11, App1
Sequence 11, App1
Sequence 31, App1
Sequence 31, App1
Sequence 32, App1
Sequence 33, App1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        (without alignments)
47.436 Million cell updates/sec
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/cgn2_f/ptodatta/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_f/ptodatta/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOG_NEW_PUB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOZ_NEW_PUB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOZ_PUBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOZ_PUBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_PUBCOMB.pep:*
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/cgn2_f/ptodatta/1/pubpaa/USOB_UBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_UBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_UBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_UBCOMB.pep:*
/cgn2_f/ptodatta/1/pubpaa/USOB_UBCOMB.pep:*
                                                                                                                                   May 12, 2003, 15:38:52 ; Search time 1.94 Seconds
version 5.1.4_p5_4578 - 2003 Compugen Ltd.
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US-09-982-172-152
US-09-822-172-152
US-09-826-290-464
US-09-900-936-11
US-09-900-936-11
US-10-074-956-5
US-110-015-979-63
US-110-015-979-71
US-09-803-864-9
US-09-803-864-9
US-09-803-864-9
US-09-803-864-9
US-09-803-864-9
US-09-803-918-6
US-09-850-061A-31
US-09-850-061A-33
US-09-850-061A-33
US-09-850-061A-33
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Maximum Match 100%
Listing first 45 summaries
                                                                                         using sw model
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  GenCore
(c) 1993
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seq length: 200000000
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Match Length
                                                                                         protein search,
                       Copyright
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                    score:
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Maximum DB
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                                                                                                                                 Run on:
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APPLICANT: Emil Israel Katz
TITLE OF INVENTION:
TITLE OF INVENTION: DEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBO
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Entl Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBO
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
FILLE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
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Sequence 11,
Sequence 25,
Sequence 25,
Sequence 25,
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   Sequence 19,
Sequence 10,
Sequence 25,
Sequence 47,
Sequence 58,
Sequence 84,
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Sequence
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Sequence
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US-09-972-475-19
US-09-895-443-10
US-09-982-172-47
US-09-982-172-58
US-09-982-172-84
US-09-982-172-84
US-09-982-172-84
US-09-982-172-84
US-09-982-172-84
US-08-837-659-17
US-08-839-248-3
US-08-839-248-3
US-08-839-248-3
US-08-839-248-3
US-08-839-248-3
US-08-839-248-3
US-08-899-694-15
US-08-898-92
US-08-987-699A-15
US-08-987-699A-15
US-08-987-699A-16
US-08-808-031A-52
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Pred. No. 3e+05;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 145, Application US/09982172 Patent No. US20020137119A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 152, Application US/09982172 Patent No. US20020137119A1
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larity 100.0%;
Conservative 0;
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2001-10-19

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APPLICANT: White, Frost
APPLICANT: White, Frost
TITLE OF INVENTION: Nucleic acid Molecules, Polypeptides and
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Alzheimer's Disease
TITLE OF INVENTION: Alzheimer's Disease
CURRENT APPLICATION UNBER: US/09/826,290
CURRENT APPLICATION UNBER: 2001-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09900936
Patent No. US20020165141A1
GENERAL INFORMATION
APPLICANT: Rodgers, Kathleen
APPLICANT: dizerega, Gere
APPLICANT: dizerega, Gere
TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
TITLE OF INVENTION: or Differentiation
FILE REFERENCE: 00-506-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:AII (1-3) US-09-900-936-11
                                                                                                                                                                                                                          : Durham, L.Kathryn
: Friedman, David L.
: Herath, Herath Mudiyanselage Athula Chandrasiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 4;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/900,936 CURRENT FILING DATE: 2001-07-09 NUMBER OF SEQ ID NOS: 50 SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/194,504
                                                                                                                                                            Application US/09826290
                                                                                                                                                                                                                                                                                                                                                                                                                                                ownsend, Robert Reid
                                                                                                                                                                                                                                                                                               Lida H.
Rajesh Bhikhu
                                                                                                                                                                                                                                                                                                                                                                                                                                Sunderland, P. Tre
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                                                                                                                                                                                                                                                                                                                                                                                     Silber, B. Michael
Stiger, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                Christian
                                                                                                                                                                                                                                                                                                                                         David M.
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; ORGANISM: homo sapien
US-09-826-290-464
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Best Local Similarity
Matches 1; Conserv
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US-09-900-936-11
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REAGENTS AND METHODS FOR THEIR USE
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                                                                                                                                                                                                                                                 Length 2;
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                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
                                                                                                                                                                                                                                               DB 10;
3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D377/AP6D
                                                                                                                                                                                                                                      100.0%; Score 4;
ilarity 100.0%; Pred. No.
Conservative 0; Mismatral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: STRESH M. DESAI
APPLICANT: THOMAS P. LERAY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI I. BUIJK
APPLICANT: ISA K. MOSHAMMY
TITLE OF INVENTION: NON A, NON-B, NO
TITLE OF INVENTION: REAGENTS AND ME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plication US/08424550B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: ABBOTT LABORATORIES
: 100 ABBOTT PARK ROAD
ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435435
TTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 5:
FELECOMMUNICATION INFORMATION
TELEPHONE: 708-937-6365
CURRENT FILING DATE: 2001-10-1
NUMBER OF SEQ ID NOS: 253
SOFWARE: Patentin version 3.1
SEQ ID NO 152
LENGTH: 2
                                                                                                              TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20119447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 1; Conserv
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ZIP: 60064-3500
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STATE:
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Gaps

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OTHER INFORMATION: Description of Artificial Sequence: CB4 domain of mutant 18
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                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Motif 4, corresponding to residues 188 to 190 of
; OTHER INFORMATION: SEQ ID NO:2
US-10-039-8768-6
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                               PPLICANT: Blumberg, Hal
ITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, 2219A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 4; DB 9;
Pred. No. 3e+05;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 4; DB 9; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                        CURRENT APPLICATION NUMBER: US/10/039,876A
                                                                                                             CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 60/061,712
PRIOR FILING DATE: 1997-10-06
PRIOR FLING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PastSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Verhaert, Raymond M.D.
APPLICANT: Beekwilder, Martinus J.
APPLICANT: Aehle, Wolfgang
TITLE OF INVENTION: Enzyme Selection
FILE REFERENCE: 2183-52070S
CURRENT APPLICATION NUMBER: US/10/015,979
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PRIOR APPLICATION NUMBER: PCT/NL00/00399
PRIOR FILING DATE: 2000-06-09
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PRIOR APPLICATION NUMBER: 60/138,443
PRIOR FILING DATE: 1999-06-10
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US-10-015-979-71
; Sequence 71, Application US/10015979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 63, Application US/10015979; Publication No. US20030036050A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.1
SEQ ID NO 63
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ORGANISM: Artificial Sequence
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                                                                      ILE REFERENCE: 97-63C1
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Best Local Similarity
Matches 1; Conservat
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Matches 1; Conserv
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; OTHER INFORMATION:
US-10-015-979-63
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Designed polypeptide with anti-inflammatory, anti-bacterial, anti; OTHER INFORMATION: -fungal and antipyretic properties.
US-09-828-272A-1
                                                                                                                                                                                                                                                                               APPLICANT: LIFTON, James M
APPLICANT: LIFTON, James M
APPLICANT: CATANIA, Anna P
TITLE OF INVENTION: USE OF KPV TRIPEPTIDE FOR DERMATOLOGICAL DISORDERS
FILE REFERENCE: 239/058
CURRENT APPLICATION NUMBER: US/09/828,272A
CURRENT APPLICATION DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
                           Gaps
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  Pred. No. 3e+05;
; Mismatches 0; Indels
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TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFERENCE: 08191-022001
CURRENT APPLICATION NUMBER: U5/10/074,956
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASTSEQ for Windows Version 4.0
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100.0%; Pred. No. 3e+05;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                    Sequence 1, Application US/09828272A Publication No. US20020183255A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10074956
Publication No. US20020193332A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Matches 1; Conservative 0
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US-10-074-956-5
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Best Local Similarity
Matches 1; Conserv
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US-10-039-876A-6
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APPLICANT: Rodgers, Rathleen
APPLICANT: discrega, Gere
TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
FILE REFERENCE: 99-1043-A
CURRENT APPLICATION NUMBER: US/09/7711,192
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 3
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APPLICANT: Chu, Ivan K.
APPLICANT: Chu, Ivan K.
APPLICANT: Lau, Tai-Chu
APPLICANT: Siu, K. W. Michael
ITILE OF INVENTION: Sequencing of Peptides by Mass Spectrometry.
FILE REFERENCE: 7933.208-US-UI
CURRENT APPLICATION NUMBER: US/09/804,866
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 60/193,208
PRIOR PILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 3
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; OTHER INFORMATION: Description of Artificial Sequence:AII (1-3) US-09-771-192-11
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Patent No. US20020049162A1
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100.0%;
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; OTHER INFORMATION: X is Q or
US-09-804-866-14
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bovine ubiquitin
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Best Local Similarity
Matches 1; Conserv
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Matches 1; Conserv
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US-09-853-918-6
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APPLICANT:
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PPPLICANT: Kim E. Leitzel
IITLE OF INVENTION: Sensitive Detection of Wild-Type and
IITLE OF INVENTION: Manate EGFR by Specific ELISA Assays in Any Biological
IITLE OF INVENTION: Sample
IITLE OF INVENTION: Sample
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red. No. 3e+05;
Mismatches 0
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SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 3
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Pred. No.
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/015,979
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CURRENT FILING DATE: 2001-03-12
                                                                                                                                                                                                          CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: PCT/NL00/00399
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/138,443
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.1
                                                               APPLICANT: Quax, Wilhelmus J.
APPLICANT: Verhaert, Raymond M.D.
APPLICANT: Beekwilder, Martinus J.
APPLICANT: Aehle, Wolfgang
TITLE OF INVEWIION: Enzyme Selection
FILE REFERENCE: 2183-52070S
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PRIOR FILING DATE: 2000-03-10
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Patent No. US20010046686A1
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APPLICANT: Albert J. Wong
APPLICANT: David K. Moscatello
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illarity 100.0%;
Conservative 0
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                         US20030036050A1
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US-09-803-854-9
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Best Local Similarity
Matches 1; Conserva
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Best Local Similarity
Matches 1; Conserv
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; LOCATION: (1)..(3)
; OTHER INFORMATION:
US-10-015-979-71
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US-09-804-866-14
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RPLICANT: TSERNIGS, Lars
ITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
ILLE REFERENCE: 033315-002
                                                    TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
FILE REFERENCE: DB124MP
CURRENT APPLICATION NUMBER: US/09/853,918
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,448
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 6
LENGTH: 3
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CURRENT PEDILOCATION NUMBER: US/09/850,061A
PRIOR APPLICATION NUMBER: US 09/095,106
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1996-12-09
PRIOR APPLICATION NUMBER: PCT/SE96/01621
PRIOR APPLICATION NUMBER: PCT/SE96/01621
PRIOR APPLICATION NUMBER: US 9504467-3
PRIOR FILING DATE: 1995-12-12
PRIOR PILING DATE: 1995-12-12
PRIOR SED ID NOS: 44
NUMBER OF SED ID NOS: 44
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Mouravieff, Julie E.
Einspahr, Howard M.
Kish, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NORDSTEDT, Christer
APPLICANT: NASLUND, Jan
APPLICANT: THYBERG, Johan
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1larity 100.08;
Conservative
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; ORGANISM: Homo sapiens
US-09-853-918-6
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; ORGANISM: Amyloidosis
US-09-850-061A-31
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Best Local Similarity
Matches 1; Conserva
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Search completed: May 12, 2003, 15:59:10 Job time: 2.94 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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	Description	· o	phenol 2-monoaxyge	22K superhelical D	cell surface adhes	hypothetical prote	al pro	glucan 1,4-alpha-q	hypothetical prote	schwannomin - mous	branched-chain-ami	glycogen phosphory	peptidyl-dipeptida	copper resistance	R-phycoerythrin al	anglotensin-conver	hypothetical prote			fulicin - giant Af	cocoonase (EC 3.4.	myosin light chain	phosphoprotein, bo	Iq heavy chain CRD	27.5 kda structura	27.5K structural p	27.5K structural p	28.5K structural p	28K structural pro	alcohol dehydrogen
SUMMARIES	ΩI	PQ0010	A37832	A61300	B43848	T46627	S17255	A27897	T30569	I54357	A40135	A60521	JN0862	C41225	B22565	PQ0009	T14908	T14910	S55237	A44692	B61168	150385	S11127	PT0278	G44817	144817	E44817	C44817	A44817	S66195
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RESULT 3

alcohol dehydrogen peptidy-dipeptida RNA-directed DNA p dnaA protein - pse N'formyl oligopept hydrogensulfite re angiotensin-conver sperm acrosomal pr contraction-inhibi contraction-inhibi glycoprotein compo ribosomal protein transferrin - bovi whey glycoprotein acylaminoacyl-pept alpha-1,4-glucan-p	ALIGNMENTS itor (FLP-3) - common fig ide 3) ion 15-Jun-2001 #text_change 15-Jun-2001 H. 989 nzyme inhibitors derived from Ficus carica. enzyme inhibitor	ore 4; DB 3; Length 3; ed. No. 0; Mismatches 0; Indels 0; Gaps 0;	use (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragnas sp. #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993 ngler, V. 1834-6840, 1990 alyseptide requirements of multicomponent phenol hydro A37832; MUD:91072231; PMID:2254259 Yetein Py Loctase	ore 4; DB 2; Length 4; ed. No. 0; Mismatches 0; Indels 0; Gaps 0;
\$02617 A35890 B34835 A60986 \$11024 \$00008 A61140 A77696 B27696 H48394 A197764 A197764 A197764 A197764 B26206	ALIGN Inhibitor () Inhibitor () In flg) revision 15 anaka, H. 67, 1989 ing enzyme	Sc. Pr.	1.14.13.7) chain ce_revision.14-Ju V. 0, 1990 of polypeptide ru MUID:91072231; 1	Sc. Pr.
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কবৰককৰ কৰা কৰা কৰা কৰা কৰা কৰা কৰা কৰা কৰা	RESULT 1 PQ0010 angiotensin-converting enzyme inhibiton NiAlternate names: fitus latex peptide C:Species: Flcus carica (common fig) C:Date: 15-Jun-2001 #sequence_revision C:Accession: P00010 C:Accession: P0	Match local 1 v l 1 v l 2 v 2		atch cal
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mitochondrial, questionable - yeast (Saccharomyces cerevisiae
                                                                                                                                                                                                                                                           A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit fr
A;Reference number: S17255; MUID:91285106; PMID:2060626
A;Accession: S17255
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Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Asper
A;Reference number: 220869; MUID:99087906; PMID:9871120
                                                                                                                                                                                                            R;Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa,
FBBS Lett. 284, 51-56, 1991
                                                                                                                                                                                                                                                                                                                                                                                              ;Comment: A coding region for this protein could not be identified in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Inokuchi, N.; Takahashi, T.; Irie, M.
J. Balcohen. 90, 1055-1067, 1981
A;Title: Purification and characterization of a minor glucoamylase from Aspergillus A;Reference number: A27897; MUID:82075730; PMID:6796572
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T30569
                                                                                                                                                              C;Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
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C;Keywords: mitochondrion; protein biosynthesis; ribosome
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A;Molecule type: DNA
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                                                                       C; Accession: A61300
R; Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
B; Schina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
B; Stocham. 92, 1059-1068, 1982
A; Title: Purification and characterization of a protein from Escherichia coli which form A; Reference number: A61300; MUID: 83082696; PMID: 6294066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: T46627
R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A; Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
                                                                                                                                                                                                                                                           A;Residues: 1-4 <KIS>
C;Comment: This protein resembles some of the histone-like protein of bacteria in amino
C;Reywords: DNA binding; monomer
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                                           17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
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Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
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perhelical DNA-binding protein - Escherichia coli (fragment)
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A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings
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A;Note: sequence extracted from NCBI backbone (NCBIP:85444)
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Affilie: Binding of heparan sulfate to Staphylococcus aur. A; Reference unmber: A43848; MUID:92176005; PMID:1541563
A; Accession: B43848
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A;Molecule type: protein
A;Residues: 1-4 <LIA>
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A; Experimental source: intestine C; Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-conve C; Superfamily: bradykinin-potentiating peptide C; Keywords: anglotensin-converting enzyme inhibitor
    A;Residues: 1-5 <BON>
C;Superfamily: phosphorylase
C;Reywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status expe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
A;Reference number: JN0859; MUID:94080036; PMID:7764272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: C41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer
A;Reference number: A41225; MUID:92020961; PMID:1924351
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C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0862
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A; Molecule type: protein
A; Residues: 1-5 < CHA>
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                                                                                                                                                                                                                                                                                                                           R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Mum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are cd
A;Reference number: I54357; MUID:95072570; PMID:7981675
A;Accession: I54357
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N'Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Blochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A;Reference number: A60521; MUID:90227907; PMID:2109669
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N/Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
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C;Date: 02-Aug_1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
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Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
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A;Cross-references: GB:L28838; NID:g454836; PIDN:AAA57150.1; PID:g601923
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C;Accession: A40135
R;Hutson, S,M.; Wallin, R.; Hall, T.R.
submitted to the Protein Sequence Database, March 1992
A;Reference number: A40135
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A;Molecule type: mRNA
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A Molecule type: protein
A? Residues: 1-4 < HUT>
C; Keywords: aminotransferase; mitochondrion
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Matches 1; Conservative 0;
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A; Molecule type: protein
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Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Recession: PQ0009
                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N;Alternate names: flcus latex peptide 2
C;Species: Flcus carica (common fig)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C;Accession: PQ0009
A,Title: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A2565; MUD:85182601; PMID:3886644
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>
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A; Residues: 1-5 <MAR>
A; Experimental source: latex
C; Keywords: anglotensin-converting enzyme inhibitor
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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on: May 12, 2003, 15:32:07 ; Search time 0.58 Seconds

(without alignments)

71.511 Million cell updates/sec
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Title: US-09-909-348-4

Perfect score: 4
Sequence: 1 V 1
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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TISSUE-Skin secretion;
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
"Tyler M.J., Wallow G. J.C.,
"The structure of new peptides from the Australin red tree frog
"Intoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
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Wabhitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                       5 AMIDATION.
5 AA; 616 MW; 61F2D1A059A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Rubellidin 3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA.
                                                                                                                                                                                                           100.0%; Score 4; DB
100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 4; 100.0%; Pred. No.
rubella.";
Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: SECRETED.
Amphibian skin; Amidation.
'An PRS 5 5 AMIDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                            Local Similarity
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Best Local Similarity
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P82070;
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                                "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.";
FEBS Lett. 284.51-56(1991).
PIR; S17255; S17255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
NCBI_TaxID=104895;
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria
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                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                            100.0%; Score 4; DB 1; Length 4; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                      4 AA; 402 MW; 7771B2D5D000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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-!- SUBCELLUIAR LOCATION: SECRETED.
Amphibian skin; Amidation.
MOD RES 5
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                                                                                                                                                                                Ribosomal protein; Mitochondrion.
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                                                                                                                                                  L0002681; MRPL1
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Matches 1; Conserv
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Matches 1; Conserv
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        Kitakawa M.;
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P82100;
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SEQUENCE

Query Match

RESULT 4 EI04_LITRU

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Panicoldeae; Andropogoneae; Zea.
NCBI_TaxID-4577;
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Best Local Similarity
Matches 1; Conserv
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P25154;
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SEQUENCE
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98163340; PubMed-9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate.
--- PATHRAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHRAYS.
---- SUBUNIT: HOMODIMER (BY SIMILARITY).
---- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
HSC-2DPAGE; P54714; DGG.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Ćhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electrophoresis 18:2795-2802(1997).
-1- CATALYTIC ACTIVITY: D-91yceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000652; Triophos_ismrse.
PROSITE; PS00171; TiM; PARTIAL.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
Pentose shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
rubella.";
Aust. J. Chem. 52:639-645(1999).
-1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS Amphibian skin.
                                                                                                 DB 1; Length 5;
0;
                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5;
                                                                                                                                                                                                                                                            01-CCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
                                                                          5 AA; 570 MW; 71A9C9C862A00000 CRC64;
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                                                                                                                         0; Mismatches
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                                                                                                 100.0%; Score 4; 100.0%; Pred. No.
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                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
                                                                                                 Query Match
Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       rissue-Heart;
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P80628;
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SEQUENCE
                                                                          SEQUENCE
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UC22_MAIZE
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
(APH) (Acylaminoacyl-peptidase) (Fragment).
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"N-terminal sequence analysis of N alpha-acetylated proteins after
unblocking with N-acylaminoacyl-peptide hydrolase.";
Anal. Blochem. 199:45-50(1991).
-I- FUNCTION: THIS ENZYME CATALZES THE HYDROLYSIS OF THE AMINO-
TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER
                                                                                    genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-I- MISCELLANEOUS: ON THE 2DE THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
Malze-2DPAGE; P80628; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Walvaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                             654 MW; 72CB19C9C0300000 CRC64;
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
MEROPS; S09.004; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AA.
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PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
Hydrolase; Acetylation.
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01-MAY-1992 (Rel. 22,
15-JUN-2002 (Rel. 41,
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Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance plasmid, pCF10.";
J. Biol. Chem. 253:14574-14578(1988).
-!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PCF10.
                                                                                                                                                                                                                                                                            Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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"Structure of CCFIO, a peptide sex pheromone which induces conjugative transfer of the Streptococcus faecalis tetracycline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 4; DB 1; Length 6; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels
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6 AA; 792 MW; 6683704772C9A000 CRC64;
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                                      P82096;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
6 AA.
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-1- SUBCELLULAR LOCATION: SECRETED.
Amphibian skin; Amidation.
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STANDARD;
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nes 1; Conser
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ID WWA1_ACHFU
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-i- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
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Biochem. Biophys. Res. Commun. 152:1376-1387(1988)
-!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
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                                                                                                                         01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
Contraction-inhibiting peptide I (MIP I).
Mytilus edulis (Blue mussel).
Edkaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloides, Mytillidae; Mytilli
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Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
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72C9C6876DD81000 CRC64;
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(Rel. 13, Last sequence update)
(Rel. 37, Last annotation update)
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MEDLINE-88240357; PubMed-3377776;
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MEDLINE-88240357; PubMed-3377776;
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NCBI_TaxID-6550;
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-1- SIMILARITY: TO MIP I.
PIR; B27696; B27696.
Hormone; Amidation.
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Wakanide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
                                                                                                                                                                                                                                                                                          S Lett. 323:104-108(1993).
FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
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Wamaidel., -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
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7 AA; 993 MW; 7362D5B69B041310 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
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MEDLINE-93265912; PubMed-8495720;
                1-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last seq
1-OCT-1994 (Rel. 30, Last anno
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X MEDLINE-91282758; PubMed-1840486;

A Sato H., Aono S., Rashiwamata S., Kolwal O.;

A Sato H., Aono S., Rashiwamata S., Kolwal O.;

Sato H., Aono S., Rashiwamata S., Kolwal O.;

Genetic defect of bilitubin UDP-glucuronosyltransferase in the hyperbilitubinemic Gunn rat.";

L Blochem. Blophys. Res. Commun. 177:1161-1164(1991).

C -I FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND ENDGENOUS COMPOUNDS.

C -I CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR BETA-D-GLUCORONOSIDE.

C -I SUBCELLULAR LOCATION: MICROSOME.

REMBL; S38636; AAB19259.1; -
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID-10116;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
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Kraig E.;
"cis Elements and trans factors are both important in strain-specific
regulation of the leukotoxin gene in Actinobacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                         Actinobacillus actinomycetemcomitans (Haemophilus actinomycetemcomitans).
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Actinobacillus.
NCBI_TaxID=714;
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88298; AAB66311.1; -.
                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last an
Catechol-2,3-dloxygenase (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actinomycetemcomitans.";
Infect. Immun. 64:3451-3460(1996).
EMBL; U51862; AAB88721.1; -.
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MEDLINE-96355846; PubMed-8751884;
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01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sphingomonas chungbukensis
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L'aga 1; Conservat
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Best Local Similarity
Matches 1; Conserv
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NCBI_TaxID-56193;
                                                                                                          GlyA (Fragment)
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01-JAN-1998 (
01-DEC-2001 (
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SEQUENCE
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P70804
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034028
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Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
*Organization and expression of nitrogen-fixation genes in the aerobic
nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
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MEDILINE-94079349; Pubmed-8257126;
Rather P.N., Mann P.A., Merzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the aac(3)-Via gene encoding a novel 3-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                             Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801).
Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
NCBL_TaxID=41431;
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Enterobacter.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Antimicrob. Agents Chemother. 37:2074-2079(1993).
EMBL; M88012; AAA16193.1; -.
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                                                                                                                                   PRT;
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EMBL; AF003700; AAC35193.1; -.
NON_TER 1
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Best Local Similarity
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"Characterization of the cmcH genes of Nocardia lactandurans and Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem 0-cardamoyltransferase for cephamycin biosynthesis."; Gene 162:21-27(1995).

EMBL: Z21682; CAA79797.1; -.
       Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
NCBI_TaxID=1913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
BYPOCHACLICAL 0.7 kDa protein (Fragment).
DIDI 10A-2B.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                          SEQUENCE FROM N.A.
MEDLINE-96009872; PubMed=7557411;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L.,
                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 4; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 6.6e+05; Matches 1; Conservative 0; Mismatches 0; Indels
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Q95945;
Q1-FEB-1997 (TrEMBLrel. 02, Created)
Q1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Inside intron 5 (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                          7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
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EMBL; V00694; CAA24066.1; -.
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                                                                                                                                                                                  Rehm B.H.A., Ertesvag H., Valla S.,
A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.",
J. Bacteriol. 178:5884-5889(1996).
EMBL, X87973; CAA61230.1;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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"Analysis and regulation of the sec Y gene from Streptomyces griseus N2-3-11 and interaction of the SecY protein with the SecA protein.";
Blochim. Blochim. Acta 1447:298-302(1999).
EMBL; X95915; CAA65160.1;
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                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 6.6e+05;
ttive 0; Mismatches 0;
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01-FEB-1997 (TrEMBLrel. 02, Last sequenc
01-DEC-2001 (TrEMBLrel. 19, Last annotat
3'-methylcephem hydroxylase (Fragment).
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MEDLINE-20011291; PubMed-10542330;
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AlgT protein (Fragment)
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                                  Azotobacter vinelandii
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Best Local Similarity
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                                                                                           NCBI_TaxID=354;
                                                                         Azotobacter
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STRAIN=FS772/70;
MEDIJNE-88216185; PubMed=2835592;
Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;
Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;
Sequence of the Nucleoprotein Gene from a Virulent British Field
Isolate of Transmissible Gastroenteritis Virus and its Expression in
Saccharomyces Cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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01-DEC-2001 (TrEMBLrel. 19, Last amonation update)
Membrane protein (1 is.3rd base in codon) (Fragment).
Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronavirus.
Norm manners.
                                                   Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtaszek P., Bolwell G.P.;
                                                                                      "Proteomic study of secondary cell wall proteins from transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
                                                                                                                                                                                                                         100.0%; Score 4; DB 10; Length 7; 100.0%; Pred. No. 6.6e+05; Live 0; Mismatches 0; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7. AA; 869 MW; 72C691E727233B70 CRC64;
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llarity 100.0%; Pred. No. 6.6e+05;
Conservative 0; Mismatches 0;
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                                                                                                                                  -1- SUBCELLULAR LOCATION: CELL WALL.
-1- TISSUE SPECIFICITY: XYLEM.
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                                                                                                                    Planta 0:0-0(2000)
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 NCBI_TaxID-4097;
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Blee K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum (Tomato).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
                                                                       Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.; "Arabidopsis thaliana genes expressed in the early compatible interaction with root-knot nematodes.";
Mol. Plant Microbe Interact. 14:288-299(2001).
EMBL; AJ286350; CAB71014.2;
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Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
10 kDa cell wall protein (Fragment).
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7 AA; 828 MW; 71B412C7377415D0 CRC64;
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NCBI_TaxID-3702;
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Crawford-Hiksza L.K., Nang R.N., Schnurr D.P.;
Myolecular surveillance of Errain variation in adenoviruses causing acute respiratory disease, Av 4 and Av 7a.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065066; AAD036681;
EMBL; AF065066; AAD036661;
EMBL; AF065067; AAD0366611; -.
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=85755;
MEDLINE-99175282; PubMed-10074533; Crawford-Miksza L.K., Nang R.N., Schnurr D.P.; Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease."

J. Clin. Microbiol. 37:1107-1112(1999).
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Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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Crawford-Miksza L.K.;
Crawford-Miksza L.K.;
Crawford-Miksza L.K.;
EMBL: AF065062.10 to the EMBL/GenBank/DDBJ databases.
EMBL: AF065062.10 to the EMBL/GenBank/DDBJ databases.
NON_TER 1 1 SEQUENCE 7 AA: 980 MW; 7B5EA414140322A0 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PVI core protein (Fragment).
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STRAIN-KN T96-0620,
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